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(54) Title: **GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES**

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.



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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have served a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex); wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
10 libraries and

c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences
15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by
20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particular useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

5 The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

10 The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

15 The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation
20 table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ;
25 SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ;
SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ;
SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No :
63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No :
87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID
30 No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ;
SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No :
116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ
ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ;
SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14
10 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

 The invention relates also to a method of detecting
differentially expressed genes correlated with a cancer
25 comprising detecting at least one library of polynucleotide
sequences as above defined or of products encoded by said
library in a sample obtained from a patient.

 A particular embodiment of the invention relates
30 to a polynucleotide library of corresponding substantially to
any combination of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets 1 to set 212 as defined in
table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

30

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from anthracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an anthracycline-sensitive tumor from patients having an anthracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination
20 of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF α 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples ($n = 35$) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones ($n = 162$) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a
15 tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to
20 expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values
25 is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than
30 the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
	1	2	3	4	5	6	7	8	9	10	11	12
Tumor position in the cluster	46	58	60	63	51	58	46	47	50	47	46	66
Age, years	1	0	0	16	13	37	10	4	1	2	0	0
Nodal status	60	20	26	35	20	30	27	25	30	25	20	22
Histological size, mm												
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFBR3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XPB1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes
15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SRT No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region Y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to anthracycline from tumors unsensitive to anthracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

10 Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (Li-Fraumeni syndrome) (TP53)	206314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	128233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	248620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase p1 (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDNP2	19	actonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNP2)	120816	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selecitin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:328	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	178197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol TIK2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant 1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p80, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T65683	40	EST T65683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFB3	42	transforming growth factor, beta receptor III (TGFB3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	Insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110589	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180218	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	Villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	158979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:198	SEQ ID No:197	SEQ ID No:198
EPHA2	52	EphA2 (EPHA2)	192004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	286242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	305943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:348
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R87218	69	Est R87218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	198282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:308	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	Tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	Zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251983	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204588	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37).	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	182897		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:280	SEQ ID No:281
APC	93	adenomatous polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopa-chromatase tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	Integrin, beta 2 (antigen CD18 (p85), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	Jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1) (ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No: 164	0	SEQ ID No: 208	SEQ ID No: 209
ANXA11	110	annexin A11 (ANXA11)	158992		SEQ ID No: 165	0	SEQ ID No: 206	SEQ ID No: 207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	158909		SEQ ID No: 166	0	SEQ ID No: 212	SEQ ID No: 213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	159874	SEQ ID No: 167	SEQ ID No: 168	SEQ ID No: 173	SEQ ID No: 174	SEQ ID No: 175
BTF3L3	113	basic transcription factor 3 (BTF3)	185889	SEQ ID No: 169		SEQ ID No: 289	0	SEQ ID No: 290
EST R55460	114	EST R55460	154997		SEQ ID No: 170	0	SEQ ID No: 185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No: 171		SEQ ID No: 253	0	SEQ ID No: 254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No: 172	SEQ ID No: 173	SEQ ID No: 144	SEQ ID No: 145	SEQ ID No: 146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No: 174	SEQ ID No: 175	0	SEQ ID No: 183	SEQ ID No: 184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No: 176		0	SEQ ID No: 120	SEQ ID No: 121
TNFRSF8	119	tumor necrosis factor receptor superfamily, member 8 (TNFRSF8)	151767	SEQ ID No: 177	SEQ ID No: 178	SEQ ID No: 141	SEQ ID No: 142	SEQ ID No: 143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No: 179	0	SEQ ID No: 192	SEQ ID No: 193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No: 180	SEQ ID No: 181	SEQ ID No: 153	SEQ ID No: 154	SEQ ID No: 155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No: 182		SEQ ID No: 9	0	SEQ ID No: 10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No: 183	SEQ ID No: 184	SEQ ID No: 314	SEQ ID No: 315	SEQ ID No: 316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No: 185	SEQ ID No: 186	SEQ ID No: 79	SEQ ID No: 80	SEQ ID No: 81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210674	SEQ ID No: 187	SEQ ID No: 188	SEQ ID No: 319	SEQ ID No: 320	SEQ ID No: 321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1)	162246	SEQ ID No: 189	SEQ ID No: 190	SEQ ID No: 223	SEQ ID No: 224	SEQ ID No: 225
YES1	127	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No: 191		SEQ ID No: 303	0	SEQ ID No: 304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No: 192	0	SEQ ID No: 25	SEQ ID No: 26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No: 193	0	SEQ ID No: 263	SEQ ID No: 264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathpsin D (lysosomal aspartyl protéase) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363786	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300584	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	Integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S, cervicis-like 1 (HRMT1L1) (ex PRMT2))	156038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (camporelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating)	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence. Elk-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120849	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	Interleukin 3 receptor (hIL-3Re)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	Interleukin 3 receptor (hIL-3Re)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	180764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:438	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	182499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	Interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST	rien		Image ?					
AW184517								

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74; SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:78) ; SET 42: (SEQ ID No:102; SEQ ID No:103) ; SET 43: (SEQ ID No:104; SEQ ID No:105) ; SET 44: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 45: (SEQ ID No:109; SEQ ID No:110) ; SET 46: (SEQ ID No:111; SEQ ID No:112; SEQ ID No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET 49: (SEQ ID No:118; SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51: (SEQ ID No:122; SEQ ID No:78) ; SET 52: (SEQ ID No:123; SEQ ID No:124; SEQ ID No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127; SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55: (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ; SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154; SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ; SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164; SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID No:152) ; SET 69: (SEQ ID No:168; SEQ ID No:169; SEQ ID No:170) ; SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173; SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183; SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186) ; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:263; SEQ ID No:264) ; SET 111: (SEQ ID No:265; SEQ ID No:266) ; SET 112: (SEQ ID No:267; SEQ ID No:268) ; SET 113: (SEQ ID No:269; SEQ ID No:270) ; SET 114: (SEQ ID No:271; SEQ ID No:272) ; SET 115: (SEQ ID No:273; SEQ ID No:274) ; SET 116: (SEQ ID No:275; SEQ ID No:276) ; SET 117: (SEQ ID No:277; SEQ ID No:278) ; SET 118: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 119: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:284; SEQ ID No:285) ; SET 120: (SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 121: (SEQ ID No:289; SEQ ID No:290) ; SET 122: (SEQ ID No:291; SEQ ID No:292) ; SET 123: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 124: (SEQ ID No:296; SEQ ID No:297) ; SET 125: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 126: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 127: (SEQ ID No:303; SEQ ID No:304) ; SET 128: (SEQ ID No:305; SEQ ID No:306

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:
(SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID
5 No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450): SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

20 7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
10 SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ; SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96 (SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258) ; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276) ; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296; SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166 (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401) ; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424; SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184 (SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

wherein said sequences are useful in classifying good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim 20 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

33. A method of detecting differentially
5 expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

34. A method for detecting differentially
20 expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

35. A method for detecting differentially
25 expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

5

Figure 1

Normal Breast

Figure 1A

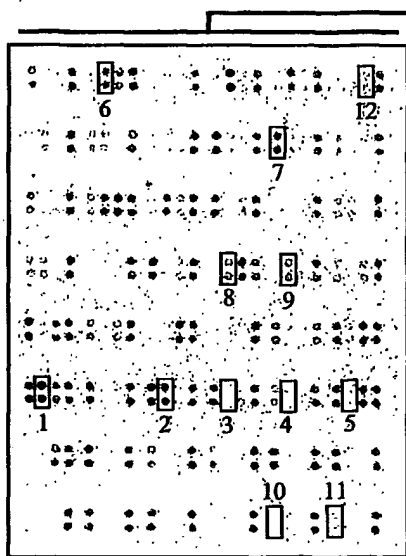
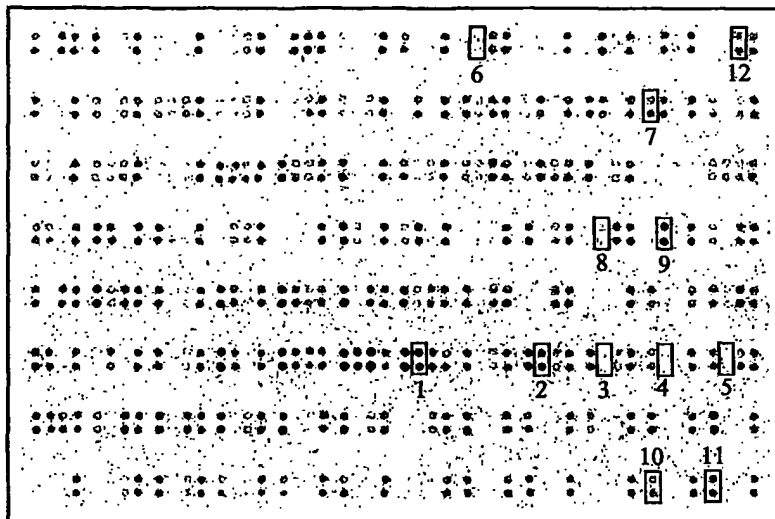
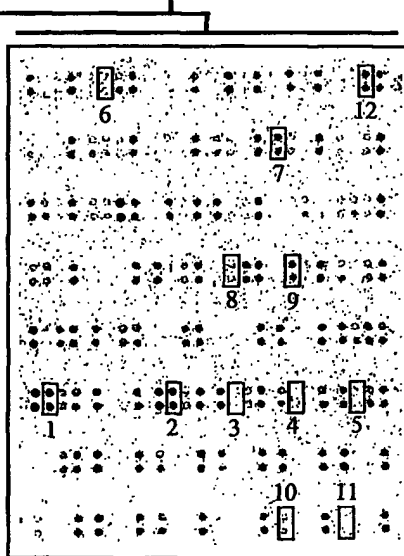


Figure 1B ER-



ER+ Figure 1C

Breast cancer

Figure 2

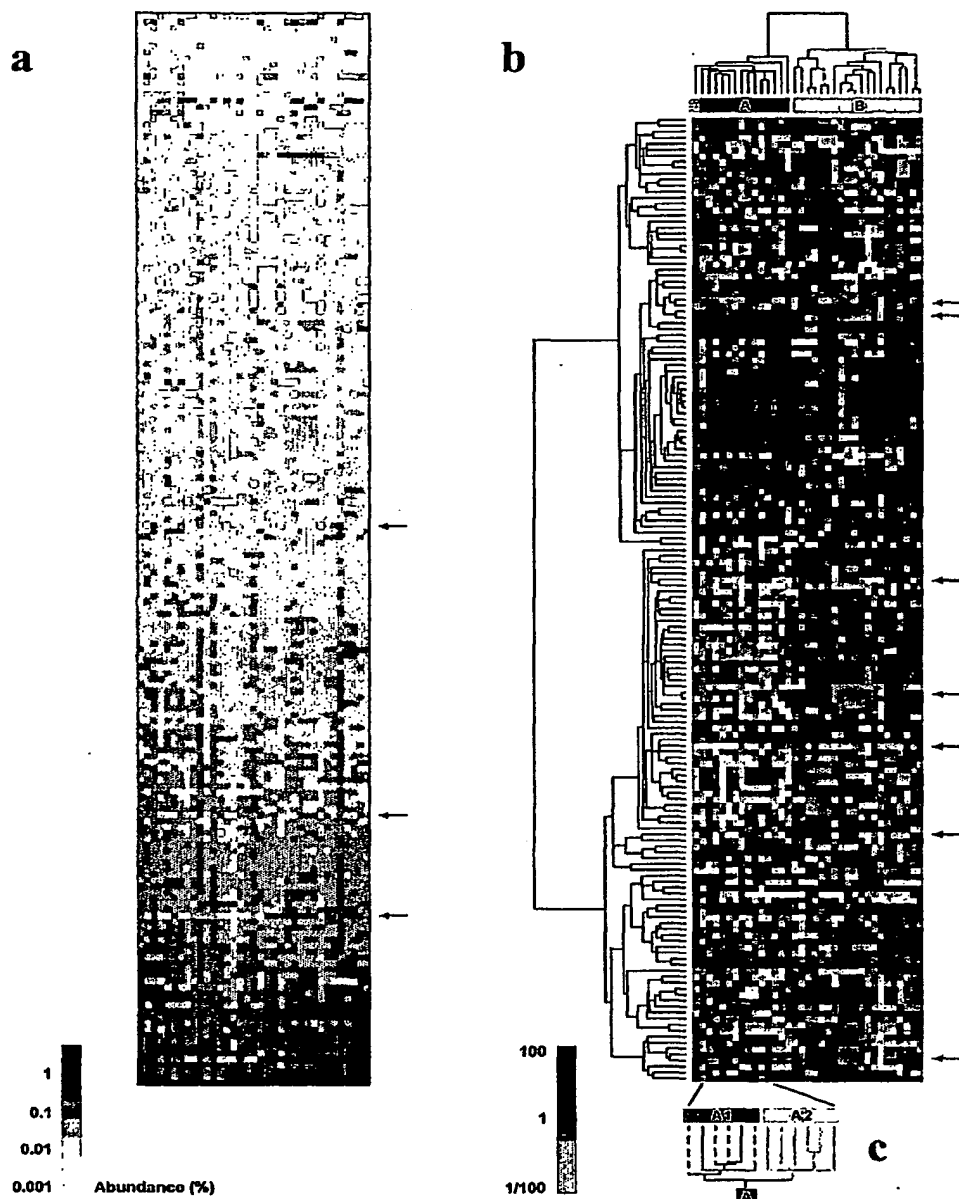


Figure 3

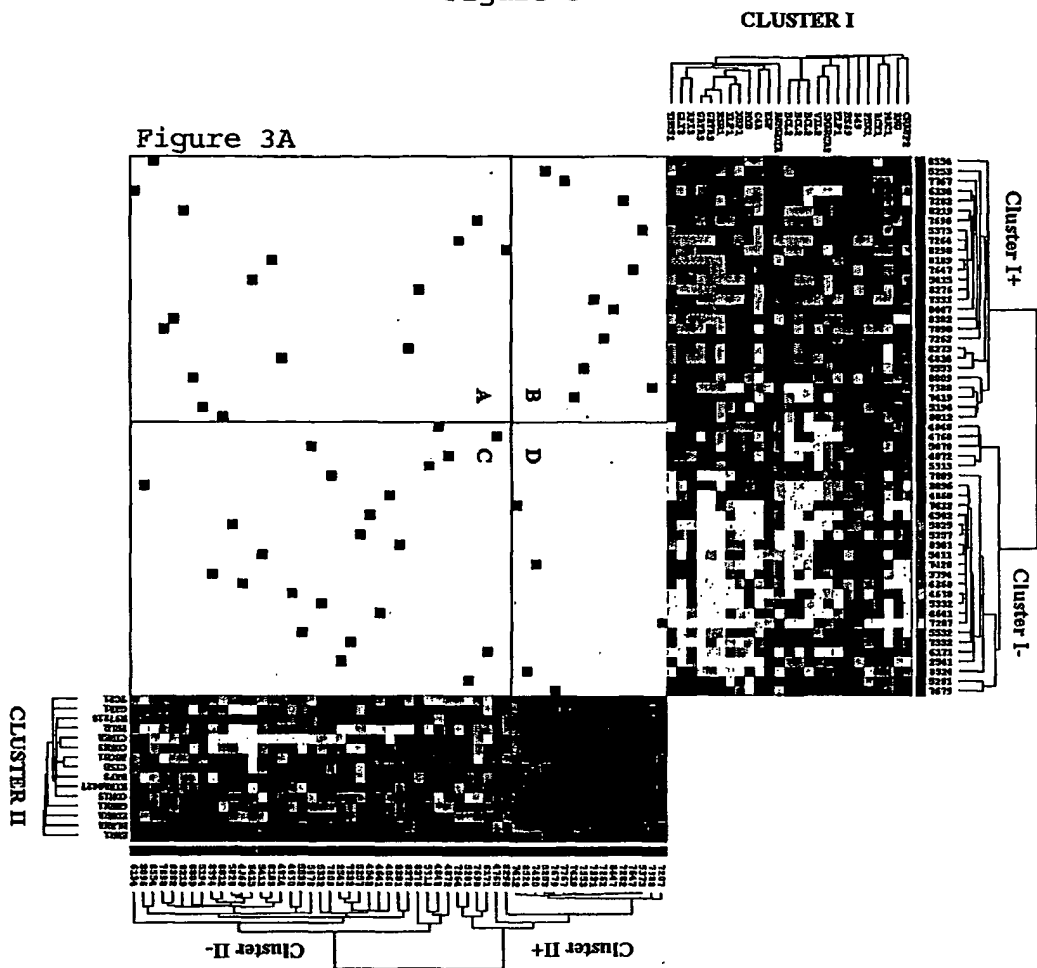


Figure 3C

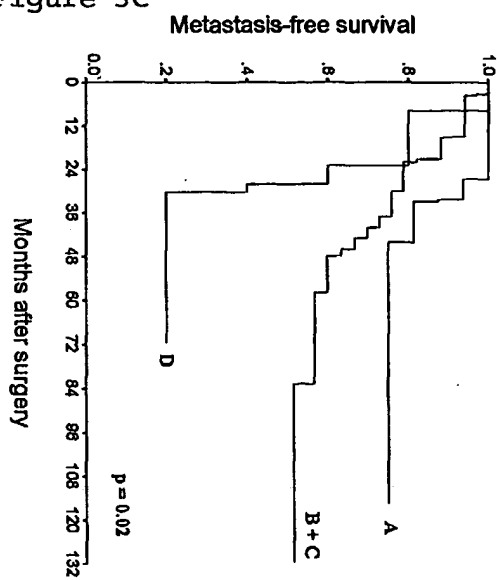


Figure 3B

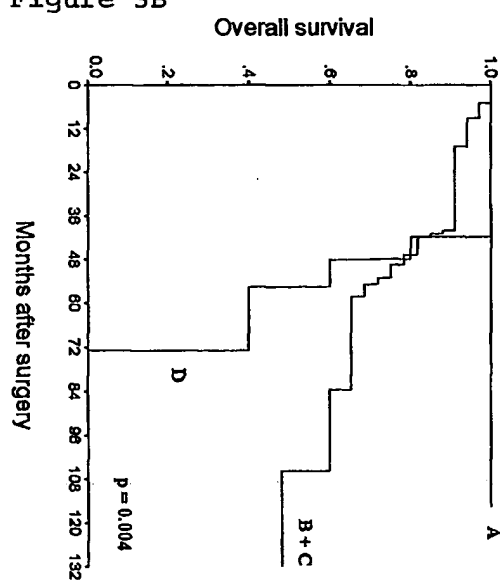


Figure 4

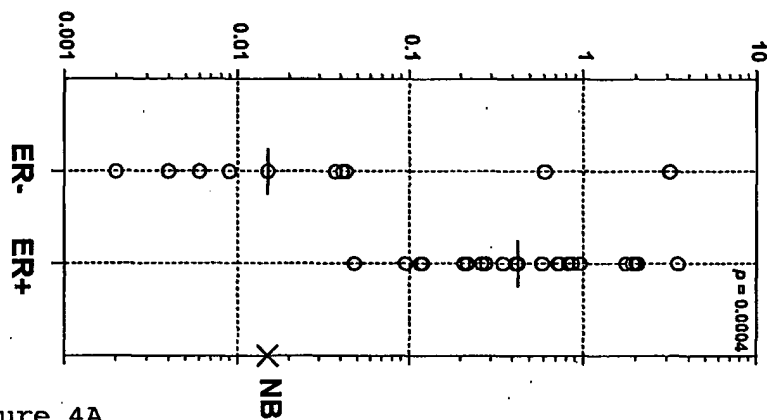


Figure 4A

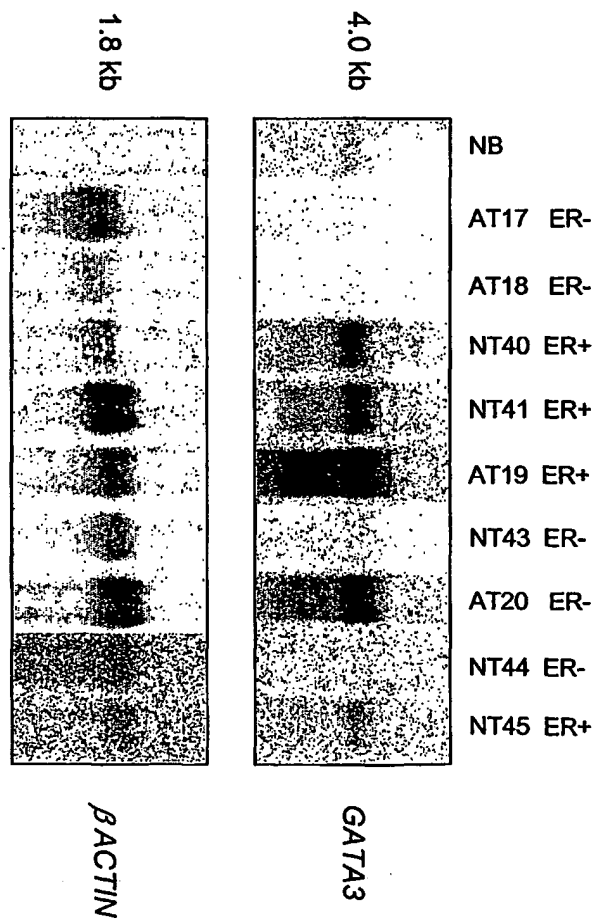


Figure 4B

SEQUENCE LISTING

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<110> François Bertucci
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Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

<120> cDNA arrays and their use for gene
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 tgatgtccag cagctggcct gtgacccta cttgttgcc caccatccgaa agtcagtctc 180
 tacaagtgc cctgctggag ctgctattgc atcaacctct gggcggtcca ataacagttc 240
 ttctaattga gactgactcc aaggccacaa actgttcaac acacacaaag tgggacaaat 300
 gggcggttca gcaggcgggt ttgggaacat aggcgaatcc gaatgggtac ttgatggaaa 360
 cctgttacca ggtgnttttt attttatttg aattttttt t nccatncctt agaggcttgg 420
 aca 423

<210> 6
 <211> 3327
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3327)
 <223> tousel-like kinase 2 (TLK2) gene.

<400> 6
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 cggcgggcggc ggcggcagca gaaatgatgg aagaattgca tagcctggac ccacgacgg c 180
 aggaattatt ggaggccagg tttactggag taggtgttag taagggacca cttaatagt 240
 agtcttccaa ccagagcttg tgcagcgtcg gatccttgag tgataaagaa gttagagactc 300
 ccgagaaaaa gcagaatgac cagcgaaatc ggaaaaagaa agctgaacca tatgaaacta 360
 gccaaaggaa aggcactcct aggggacata aaattag tga ttactttgag ttgctgggg 420
 gaagcgcgcc aggaaccagc cctggcagaa gtgttccacc agttgcacga tcctcaccgc 480
 aacattccct atccaatccc ttaccgcgac gactagaaca gccctctat ggtttagatg 540
 gcagtgtctc aaaggaggca acggaggagc agtctgtctt gccaaacctc atgtcagtga 600
 tgctagcaaa acctcggctt gacacagagc agctggcgca aaggggagct ggcctctgct 660
 tcaattttgt ttcagctcag caaaacagtc cctcatctac gggatctggc aacacagagc 720
 attcctgcag ctccccaaaa cagatctcca tccagcacag acggacccag tccgacctca 780
 caatagaaaa aatatctgca ctagaaaaa gtaagaattc tgacttagag aagaagg agg 840
 gaagaataga tgattttatta agagccaact gtgatttgag acggcagatt gatgaacagc 900
 aaaatagct agagaaatc aaggaacgat taaatagatg tgtgacaatg agcaagaaac 960
 tccttataga aaagtcaaaa caagagaaga tggcgtgtag agataagagc atgcaagacc 1020
 gcttgagact gggccacttt actactgtcc gaca cggagc ctcatctact gaacagtga 1080
 cagatgggta tgcttttcag aatcttatca agcaacagga aaggataaat tcacagagg 1140
 aagagataga aagacaacgg aaaatgttag caaagcggaa acctcctgcc atgggtcagg 1200
 cccctcctgc aaccaatgag cagaaacagc ggaaaagcaa gaccaatgga gctgaaaatg 1260
 aaacgttaac gttagcagaa taccatgaac aagaagaaat cttcaaactc agattaggtc 1320
 atcttaaaaa ggaggaagca gagatccagg cagagctgga gagactagaa aggttagaa 1380

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atctacatat cagggaaacta aaaaggatac ataatgaaga taattcacao tttaaagatc 1440
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aagtttacaa ggcatttgat ctaacagagc aaagatacgt agctgtgaaa attcaccagt 1560
taaataaaaa ctggagagat gaaaaaaagg agaattacca caagcatgca tgtagggaat 1620
accggattca taaagagctg gatcatccca gaatagttaa gctgtatgat tacttttcac 1680
tggatactga ctctgtttgt ac agtattag aatactgtga gggaaatgat ctggacttct 1740
acctgaaaca gcacaaatta atgtcggaga aagaggcccg gtccattatc atgcagattg 1800
tgaatgcttt aaagtactta aatgaaataa aacctcccat catacactat gacctcaaac 1860
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gtctttcgaa gatcatggat gatgatagct acaattcagt ggatggcatg gagctaaca 1980
cacaaggctc tggacttat tggattttac caccagagt tttgtggtt gggaaagaac 2040
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cgattcttaa agctactgaa gtgcagttcc cgccaaagcc agtagtaaca cctgaagcaa 2220
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tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtggg caaatggcgt tcagcagcgg 2460
gtttggaaac tagcgaatcc gaatggatct gatgaaacct gtaccagggt cttttatttt 2520
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ggcagctccg gccaggcctt gtaggaaaag gccccgccg aggttccagc gtcaacggcc 2640
actgtgtgtg gctgctctga gtgaggaaaa aattaaaaag aaaaactggg tccatgtact 2700
gtgaacttga aaacttgacg actcaggggg gtccctgatg cagtgttca gatgaagaat 2760
gtggacttga aaatacagac tggg ctatgc cagtgtctat atttaaactt gttcttttct 2820
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ttttgaaaga atacatttgg tcataaagtg aaaccctgat tagcaagtac gaggcaatgt 3060
tcattccaat cagatgcagc tttctctccc gtctggtctc ctgtttgcaa ttgcttccct 3120
catctcagta gggaaaaaat tgagtgggag tactgagatg tgtgggtttt tgccatttga 3180
caaagaatga ggtagaaga ctgcagcttg gagtctct ct aggttttcaa ctatttcttc 3240
acaatttgaa cacttgacgg ttgtcccttt taatttattt gaagtgcctat ttttttaaat 3300
aaaggttcat ctgtccatgc aaaaaaa 3327

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<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac agggttnnng acattgccca ggatgggtctc aaactcctag agttgagcta 60
tccaccacc tttggcctnc caaagtgtctg ggatcacagg cgtgagtcac tgtntccagc 120
accatcttg aggtcttcta aagcccaggc ccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggcccc 240
ctttgaagaa ccaactgcact gggnttttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(369)
<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tcctcttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtctttttaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt 369

<210> 9
<211> 255
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(255)
<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9
aaagacagtt tttgggtaat ctttttcttt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc ccctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc 255

<210> 10
<211> 1325
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1325)
<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

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gcagtagcag cgagcagcag agtccgcac g ctccggcgag gggcagaaga gcgcgaggga 60
gcgcggggca gcagaagcga gagccgagcg cggaccacag caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgtgcga agtggaacc 180
atccgcccgc cgtaccccca tgccaacctc ctcaacgacc ggggtgtgcg ggccatgctg 240
aaggcggagg agacctgcgc gccctcgggtg tcctacttca aatgtgtgca gaaggagggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcct gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccattcccc gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggccccagg agctgtgcga aatggagctg ctcttggtga acaagctcaa gtggaacctg 600
gccgcaatga cccgcacga ttctattgaa cacttcctct ccaaaatgcc agaggcggag 660
gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
gtgaagtcca ttccaatcc gccctccatg gtggcagcgg ggagcgtggg gccgcagtg 780
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gccctgctgg agtcaagcct gcgccaggcc cagcagaaca tggaccccaa gccgcggag 960
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gtggacatct gaggggcccc ggcaggcggg cgccaccgcc accgcagcg agggcggagc 1080
cggccccagg tgctccacat gacagtccct cctctccgga gcattt tgat accagaaggg 1140
aaagcttcat tctccttggt gttggttggt tttcctttg ctctttccc ctccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325

<210> 11

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11

atttgaaagt caaagtctta ttgataaag atgtgaatga gagaaataca gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagctc ggcggtgaa ttccggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcacgttta ctgaagagct tcactccctt agttttgaaa 240
cccaattgtg ccagcctggg ttggttaatt gacctcgaga cgacctctt gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccag cggttggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg ante tgttccttnt ttccctggact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt 449

<210> 12

<211> 4003

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

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attaaacctc tcgccgagcc cctccgcaga ctctgcgcg gaaagtttca tttgctgtat 60
gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cccttggttg 180
ggcacaaggt ggcaggatgt ctacgtggtg cgaacttcag cagcttgact caaaattcct 240
ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgggta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaat 540
tctggaaaac gccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgat 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa 720
aaccttgtag aacagagaac acgagacca tggtgtggca aagagtgatc agaacaaga 780
acagctgtta ctcaagaaga tgtatttaac gcttgacaat aagagaaagg aagtagttca 840
caaaataata gagttgctga atgtcactga acttaccag aatgccctga ttaatgatga 900
actagtggag tggaagcgga gacagcagag cgctgtatt gggggggcgc ccaatgcttg 960
cttgatcag ctgcagaact ggttcactat agttgcggag agtct gcagc aagttcggca 1020
gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac 1080
aaaaaacaaa caagtgttat gggaccgcac cttcagttt tccagcagc tcattcagag 1140
ctcgtttgtg gtggaagac agcctgcat gccaacgcac cctcagaggc cgctggtctt 1200
gaagacaggg gtccagttca ctgtgaagtt gagactgttg gtgaaattgc aagagctgaa 1260
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caccaatggc agtctggcgg ctgaatttcg gcacctgcaa ttgaaagaac agaaaaatg c 1440
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tgaaaccaa ttgtgccagc ctggttttgt aattgacctc gagacgacct ctctgcccg 1560
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gcttttgatt gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga 1920
tggtgtcatc atgggcttca tcagcaagga gcgagagcgt gccctgttga aggaccagca 1980
gccggggacc ttccctgtgc ggttcagtga gagctccgg gaagggggcca tcacattcac 2040
atgggtgagc cgggtcccaga acggaggcga acctgacttc catgcgg ttg aacctacac 2100
gaagaaagaa ctttctgtct ttactttccc tgacatcatt cgcaattaca aagtcattgg 2160
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tgcccttgga aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg 2280
ccctaaagga actggatata t caagactga gttgatttct gtgtctgaag ttcacccttc 2340
tagacttcag accacagaca acctgtccc catgtctcct gaggagtgtg acgaggtgtc 2400
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gcatcttact gaaggtaaaa ttgaaaggca ttctctgaag agtgggttcc acaagtgaag 2700
aacatccaga tacacccaaa gtatcaggac gagaa tgagg gtcccttggtg aaaggagaag 2760
ttaagcaaca tctagcaaat gttatgcata aagtcagtgc ccaactgtta taggttgttg 2820
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aattcttaca gtttttcttt gctttaagtg taactggcag ttttccattg gtttacctgt 2940
gaaatagttc aaagccaagt ttatatacaa ttatatcagt cctctttcaa aggtagccat 3000
catggatctg gtagggggaa aatgtgtatt ttattacatc tttcacattg gctattttaa 3060
gacaaagaca aattctgttt cttgagaaga gaattattgc tttactgttt gttatggctt 3120
aatgacacta gctaataatca atagaaggat gtacatttcc aaattcaca a gttgtgtttg 3180
atatccaaag ctgaatacat tctgctttca tcttggtcac atacaattat ttttacagtt 3240
ctcccaaggg agttaggcta ttcacaacca ctcatcagg agttgaaatt aaccatagat 3300
gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attaggtgtg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420

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ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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gcgaatgggt ccattctctc tcctgtactt tttccagaca cttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt tttacctttt tccttcctta tcactgacac aaaaagtaga 3660
ttaagagatg ggtttgacaa ggttcttccc ttttacatac tgctgtctat gtggctgtat 3720
cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttcttt 3780
ggtggagata aagatttctt gagttttggt ttaaaat taa agctaaagta tctgtattgc 3840
attaaatata atatcgacac agtgctttcc gtggcactgc atacaatctg aggcctcttc 3900
tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
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<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 13

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ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttatttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggggac 60
tggtggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaaac aatgaggaat acttggaact cagccaacct ctcgaacagt 180
attcacctag ttaccctgac ac aagaagtt ctgtgtcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaacatgcc ttcctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgnccccaa acagggacag gcactggggg 360
aacctaggct acattnaggc aggggaggac ccttgccttc ccaggngttt gttt 414

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<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 15
gagcgggcca gggagcgcgc gcggccgccca caaagctcgg gcgcgcgggg gctgcatgcg 60
gcgtacctgg cccggcgcgg cgactgctct c cgggctggc gggggccggc cgcgagcccc 120
gggggccccg aggcgcgagc ttgcctgcgc gctctgagcc ttgcgaactc gcgagcaaaag 180
tttggtggag gcaacgccaa gcctgagtc tttcttctc tcgttcccc aatccgaggg 240
cagcccgcgg gcgtcatgcc cgcgctctc cgcagcctgg ggtacgcgct gaagcccggg 300
aggcttggcg ccggcgaaga cccaaggacc actcttctgc gtttggagtt gctccccaca 360
accccgggct cgctcgttcc tccatcccca ccagccggg gcgcggggac aacacaggtc 420
gcggaggagc gttgccattc aagtgaactgc agcagcagcg gcagcgctc ggttcctgag 480
cccaccgcag gctgaaggca ttgcgcgtag tccatgcccg tagaggaggt g tgcagatgg 540
gattaacgtc cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
gctggggctg tttcatctgc ctggctcgtg tcacctggc aaccttgtcc ctggcccggc 660
cctcctttag tttagttgag gataccacat tagagccaga agagccacca accaaatacc 720
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tagcagactt tggactcgcc agagatatca acaatataga ctattacaaa aagaccacca 2580
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caaaattgga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
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<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaaatc tgatttggtg aattaacccc acttctcata 180
gtttaatttg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg ggttctctgag gctgctgggg gtgatcccga ggaacaagaa gctgcctat 300
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acttataggg gtagggcccc ccaaatccct cacacttagg tcggccctgc tggcttgctg 420
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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
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gtgctgaggt tacagatttc attggcccac cagcgtgtat gc tatccttt cgggggtggg 300
cattcgctca ttaattcggg cccagnccct cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttggagcac tatacccaca acactgtccg aggggtgctct tatttctaca gttaccctgc 60
agttttgtgaa tttttgcaga acaataatth actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gcccccaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcatgaata tcaggcagtt taactgttct ccacaccct actgggcttc 300
caaactttat gggatgtttt cacatgggtc tttgcctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaagt tggntcaaca ttatggntct ggatggacgg aactgatttt 420
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaagggng g ttcttcggg 480
gnntaggttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

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gcgcctccca agagagcggc cgggtgggcc tcgtcctgtc agtggcgctc gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcggg caccgctgag gagccggggc cgggcacggc 180
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cgcacgtccg gcgggctcct ggagcctgga ggaggccgag gggaccatgt ccgggaggcg 300
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<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

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<400> 20

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 tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
 aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtattttgtg caatggnacc 180
 cattattcac atgggcctag gattaaaaag tcaatttata ttnggaataa atttntccaa 240
 aaaacca 248

<210> 21

<211> 427

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(427)

<223> 5' terminal sequence. ests (EST T90726)
 gene.

<400> 21

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 gcaaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
 aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaagggtta tatttttaaag 180
 tagaataaca catgctgagt gtaaaactggg ctttggtattg gtcagctgca gtagtacaaa 240
 aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300
 aaactggcta tgtggttagga aatg atgtta aanttattgtg gggaaagttt ttcccctccn 360
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 ctttga 427

<210> 22

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(294)

<223> 3' terminal sequence. sry (sex determining
 region y)-box 4 (SOX4) gene.

<400> 22

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 cacatcaaac agtctcctct cctccacgcc tccggggtct gggaagtctc acctcactga 120
 ttccacgtag aaaagaaggc ggagggcagc agccgcgcgc ncaagctccc caacgtgcaa 180
 atccatttca gtttgaccgt gaacccctt ccagttcgtg tctcctcgc ccccgcccc 240
 tagctccgc tgctggnntc caacgggggt ntcgggtcat ttctagcgc cgg 294

<210> 23

<211> 362

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(362)
 <223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23
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 gtctccccc tcttgcaccca ccaccttggg tttgttttat tttgcttctt ggtcaagaaa 120
 ggaggggaga acccagcgca cccctccccc ctttttttaa acgcgtgatg aagacagaag 180
 gctccggggt gacgaatttg gccgatggag nat gttttgg gggaacgccg ggactgagag 240
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 cc 362

<210> 24
 <211> 2797
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2797)
 <223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24
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<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5 (RNF5) gene.

<400> 25

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tatgttttga gactgctcgg gaagctgtgg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtcccg tttatggcg agggagccag aagccccagg 240
atcccagatt aaaaactcca ccccgcccc aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatttgggt atacggggg cttccacttn ttcatttggg gt 352

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<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

```

atggcagcag cggaggagga ggacgggggc cccgaagggc caaatcgca gcggggcggg 60
gcgggcgcga ccttcgaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

```

17/292

```

gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgaggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg ccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttctcat ttggtgttgg tgcctttccc ttt ggctttt tcaccaccgt cttcaatgcc 420
catgagcctt tccgcggggg tacaggtgtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttctt gtttctcgcc atcttcttct ttttttggct gtcagtatt 540
tga 543

```

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

```

gccgtggggt gggaaagtgg gaag gtggag ttttcccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggagggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggtcttg 240
ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatntn acatagagga tttcgtcagg ctctggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

```

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

```

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcgagg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttnccggga agatttttgg gagnacacac ttttaagggc tttncctt 418

```

<210> 29

<211> 5015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

```
gagtggagtt ctggaggaat gtttaccaga cacagagccc agagggacag cggccagagc 60
ccagatagag agacacggcc tcaactggctc agcaccaggg tccccttccc cctcctcagc 120
tccctcctctg gccctttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccaggtg gccctggct ctggcctggg gggcggaggg aaagggggag ccagggggcg 240
agaaaggggt gcccaagtct gggagtggag gaaggaggca ggggtgctga gaaggcggct 300
gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcctaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cggcccgctg cccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag tttggcacc atggcgtggc ggtgccccag 480
gatgggcagg gtcccgctgg cctggtgctt ggcgctgtgc ggctgggctg gcatggcccc 540
caggggcacg caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacaggtgc 600
ccggggactc acgggcaccc ttcggtgtca gctccagggt cagggagagc ccccgagggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccaga cccaggtgcc 720
cctgggtgag gatgaacagg atgactggat agtggtcagc cagctcag aa tcacctcct 780
gcagctttcc gacacgggac agtaccagtg tttggtgttt ctgggacatc agaccttcgt 840
gtcccagcct ggctatgttg ggctggaggg cttgccttac ttcctggagg agcccgaaga 900
caggactgtg gccgccaaca ccccttcaa cctgagctgc caagctcagg gacccccaga 960
gcccgtagc ctactctggc tccagg atgc tgtccccctg gccacggctc caggtcacgg 1020
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ccataacgcc aagggggtca ccacatcccg cacagccacc atcacagtgc tccccagca 1140
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aacagtggaa agaggtgaac tggtagtcag gtaccgcgtg cgcaagtcct acagtcgtcg 1980
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gacgatgaag attgccatct gcacgaggtc agagctggag gatttcctga gtgaagcgg 2220
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tatcgccaag atgccagtca agtggattgc cattgagagt ctagctgacc gtgtctacac 2640
cagcaagagc gatgtgtggt ccttcggggt gacaatgtgg gagattgcca caagaggcca 2700
aaccocatat ccgggcgtgg agaacagcga gatttatgac tatctgcgcc agggaaatcg 2760
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gctaaatccc caggaccggc caagttttac agagctgcgg gaagatttg agaacacact 2880
gaaggccttg cctcctgccc aggagcctga cgaaatcctc tatgtcaaca tggat gaggg 2940
tggaggttat cctgaacccc ctggagctgc agggagagct gaccccccaa cccagccaga 3000
```

```

ccctaaggat tctctagatc gcctcactgc ggctgaggtc catcctgctg gacgctatgt 3060
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cccagggcag gaggatgggtg cctgagacaa ccctccacct ggtactccct ctcaggatcc 3180
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tgtgtctaag attctagatc agatgctcca agattctaga tgattaaata agattctaac 4440
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caaatgttct aagtttctaa gattctaaag gtccacaggc ctagactatt aggtgcaatt 4740
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attgttctct cctcccacac tgtgggggtg tgccccttc aagcctgtgc aatgcattag 4860
ggatgcttct tttccgagg ggatggacga tctcccacct ttggggccat gttgcccccg 4920
tgagccaatc cctcaccttc tgagtacaga gtgtggactc tgggtgcctc agaggggctc 4980
aggtcacata aaactttgta tatcaacgaa aaaaa 5015

```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)
gene.

<400> 30

```

aacacgtcac cggagagatg atgggtggcc atgcatccgc atcctgggct ggggagtgga 60
gaatggcaca ccctactggc tgg ttgcaa ctccctggaac actgactggg gtgacaatgg 120
cttctttaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggct tgcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttattc tttaagttca cgtaaggat 300
acaagtttcc agacagggtc tgaaagggtc tgggatttng gccaaacatc agacctgttc 360
tttcccaagg gaggaccaag ttctgtggct aacattcccc agcctnttgg tttaacagtt 420
gncaggacag ggcctgtt

```

20/292

<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
tccggcaacg ccaaccgctc cgctgcgcgc aggctgggct gcaggctctc ggctgcagcg 60
ctgggctggt gtgcagtggg gcgaccacg g ctcacggcag cctcagccac ccagatgtaa 120
gcatctggt tcccacctca gctcccagag tagtggtatc aggatccggc ttccaacatg 180
tggcagctct gggcctccct ctgctgcctg ctgggtgttg ccaatgcccg gagcaggccc 240
tctttccatc cctgtcgga tgagctggc aactatgtca acaaacggaa taccacgtgg 300
caggccgggc acaacttcta caacgtggac atgagctact tgaagaggct atgtggtacc 360
ttcctgggtg ggcccaagcc accccagaga gttatgttta ccgaggacct gaagctgcct 420
gcaagcttcg atgcacggga acaatggcca cagtgtcca ccatcaaaga gatcagagac 480
cagggtcctt gtggctcctg ctgggccttc ggggctgtgg aagccatct c tgaccggatc 540
tgcatccaca ccaatgcgca cgtcagcgtg gaggtgtcgg cggaggacct gctcacatgc 600
tgtggcagca tgtgtgggga cggctgtaat ggtggctatc ctgctgaagc ttggaacttc 660
tggacaagaa aaggcctggt ttctggtggc ctctatgaat cccatgtagg gtgcagaccg 720
tactccatcc ctccctgtga gcaccac gtc aacggctccc ggcccccatg cacgggggag 780
ggagataccc ccaagtgtag caagatctgt gagcctggct acagcccagc ctacaaacag 840
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gagatctaca aaaacggccc cgtggaggga gctttctctg tgtattcgga cttcctgctc 960
tacaagtcag gagtgtacca acacgtcacc ggagagatga tgggtggcca tgccatccgc 1020
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tttgacagat gcctccta at gacgcggctc aa aaggaaac caagtgggtca ggagttgttt 1860
ctgacccact gatctctact accacaagga aaatagtta ggagaaacca gcttttactg 1920
tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980
ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

```
ttccattttt cttcttttat tagaattttt tcattttttt tctcaaaatt tttatctaaa 60
aacaaacaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaa gacccctctg ggggacagca gagccagg ga cagccccccc ccacgcccag 240
cctccgtctg aggggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt cttggggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttaccaagat tggtttncca cattttccca cagcgggtaca 480
agttagtttt tg 492
```

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

```
ctnttcatgg gggactttgt ggaccgtggc ttctatagcg tcgaaacgtt nctnctgctg 60
ctggcactta aggttcgcta tctgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggtcta tggcttctac gatgagtgcg tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg cacggggggc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagagggtgg 240
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tcagagtagg tggcgacgtc cctgagacca actacctctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctc tgctgctggc acttaagggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```

22/292

```

tctacgatga gtgcctgcgc aagtacggct cggtgactgt gtggcgctac tgcactgaga 540
tcttttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
tgccatcatga tgggccatg tgtgacctcc tctggtctga cccagaagac accacaggct 720
ggggcgtag ccccgagga gccggctacc tatttggcag tgacgtggtg gccagttca 780
acgcagccaa tgacattgac atgatctgcc gtgcccacca actggtgatg gaaggttaca 840
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gtgggaatgt ggcagccatc ttggagctgg acgagcatct ccagaaagat ttcacatct 960
ttgaggctgc tccccaaag acacggggca tcccctccaa gaagcccgtg gccgactact 1020
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ctctgccatc ttctcagac ggaggctggg cgtggggggg gctgtcctgg ctctgctgtc 1140
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tgttctctct cctctctccc cacttgaacc atgaagtttc caataatttt ttttctttt 1260
tttcttctt ttttctgttt gtttttagat aaaaattttg agaaaaaaa tgaaaaaatt 1320
ctaataaaag aagaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429

```

<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests. (EST T79867)
gene.

<400> 35

```

tttttttgcc acttcagctc caaagggtgaa acggcacagt taaaagcaag aaattttgtg 60
tccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacia tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttccctac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggnac tcccngttg gatgggtntt gggggaggag ncctgntggg 480
gnnttttccc at 493

```

<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

<400> 36

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tttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgctgg ggcagcagca 120

```

23/292

gcagggggag gtntggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
 ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccg gatggggact 240
 aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
 cacggcagct cccaaggga aggggcacgg cctnngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth factor receptor 4 (FGFR4) gene.

<400> 37

atcgatgga ccgaccccc cactgcccc cagagctgta cgggctgatg cgtgagtgt 60
 ggcagcagcg ccctcccaga ggcctacett caagcagctg gtggaggcgc tggacaaggt 120
 ctgctggcgg tctctgagga gtacctcgac ctccgctga ccttcggacc ctattcccc 180
 tctggtgggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
 cctgccatt ggggattcag ctcttccct ttgggtctng gggtcagac atga gcaagg 300
 ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4) gene.

<400> 38

ccgaggagcg ctcgggctgt ctgcggaccc tgccgcgtgc aggggtcgcg gccggctgga 60
 gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaaggca gttggtggga 120
 agtccagctt ggggtccctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
 ggggtcctgc tgagtgtgcc tgggctcca gtcttgtccc tggaggcctc tgaggaaagt 240
 gagcttgagc cctgcctggc tcccagcctg gagcagcaag agcaggagct gacagtagcc 300
 cttgggcagc ctgtgcggct gtgctgtggg cgggctgagc gtggtggcca ctggtacaag 360
 gagggcagtc gcctggcacc tgctggccgt gtacggggct ggaggggccc cctagagatt 420
 gccagcttcc tacctgagga tgctggccgc tacctctgcc tggcacgagg ctccatgac 480
 gtccctgaga atctcacctt gattacaggt gactccttga cctccagcaa cgatgatgag 540
 gaccccaagt cccataggga cctctcgaat aggcacagtt acccccagca agcaccctac 600
 tggacacacc cccagcgcac ggagaagaaa ctgcatgcag tacctgcggg gaacaccgtc 660
 aagttccgct gtccagctgc aggcacccc acgcccacca tccgctggct taaggatgga 720
 caggcctttc atggggagaa ccgcattgga ggcattcggc tgcgccatca gcactggagt 780
 ctgctgatgg agagcgtggt gccctcggac cgcggcacat acacctgcct ggtagagaac 840
 gctgtgggca gcatccgcta taactacctg ctagatgtgc tggagcggtc cccgcaccgg 900
 cccatcctgc aggcgggct cccggccaac accacagccg tgggtggcag cgacgtggag 960
 ctgctgtgca aggtgtacag cgatgcccaag cccacatcc agtggtgaa gcacatcg 1020

24/292

```

atcaacggca gcagcttcgg agccgacg gt tccccctatg tgcaagtcct aaagactgca 1080
gacatcaata gctcagaggt ggaggtcctg tacctgcgga acgtgtcagc cgaggacgca 1140
ggcgagtaca cctgcctcgc aggcaattcc atcggcctct cctaccagtc tgcttggtc 1200
acggtgctgc cagaggagga cccacatgg accgcagcag cggccgaggc caggtatacg 1260
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ctcgtgagtc tagatctacc tctcgacca ctatgggagt tccccggga caggctggtg 1560
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cgacacaaga acatcatcaa cctgcttggg gtctgcaccc aggaagggcc cctgtacgtg 1800
atcgtggagt gcgcgccaa gggaaacctg cgggagttcc tgcgggccc ggcggcccca 1860
ggccccgacc tcagcccga cggctcctcg agcagtgagg ggccgctctc cttcc cagtc 1920
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atccaccggg acctggctgc ccgcaatgt ctggtgactg aggacaatgt gatgaagatt 2040
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gcgcctctcc agaggcctac cttcaagcag ctggtggagg cgtggacaa ggtcctgctg 2400
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ctcgaccttg atagcatggg gcccttggcc cagagttgct gtgcccgtgc caagggccgt 2700
gcccttggcc ttggagctgc cgtgcctgtg tcctgatggc ccaaatgtca gggttctgct 2760
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cctttcccca cactccccc tgetgctgct gccccagcgt cttgacggga gcattggccc 2940
ctgagcccag agaagctgga agcctgccga aaacaggagc aaatggcgtt ttataaa tta 3000
tttttttgaa ataaa 3015

```

<210> 39

<211> 252

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(252)

<223> 3' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 39

```

gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta 252

```

<210> 40

<211> 382

25/292

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(382)
<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40
ctnacnttca aacgganntg gaa ttatttc caaagggat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcaccggc ctgacaacga ggagagetgc 300
aatagctcag aggacgnatt caaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc 382

<210> 41
<211> 2592
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2592)
<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41
atggcaagga ggagctcggt ccagctcggt ca gataatat ccctgttcac ttttgccgtt 60
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgctg ccatgacttt gatgagctgt gtttgaagac agcccgtgcg 300
tgggagtgtg ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttgccag gggagactgc tgtaccaatt accaagtgggt ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc cttgtggcac acactctccc 600
tacatgagc cggtgtaccc aactaaaacc tttcctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgacctgt atttgatgcc 720
acttttcac tgccaggcgg agagaaattt aatcatagat ggtggggagg tcaaccgcta 780
tggattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgtgtcatc 840
cctcacgagc ggagaatatt aacctattg cagtggctca ccctgccaga tcatgagagg 900
ccttcggctc atgccttcta ttctgagcaa cctgatttct ctggacacaa atatggccct 960
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gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgcca caacagaaga 1320

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gtttataaga aaccatcagg aaaatgcttt ttccagggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
ccagctccta ataatgggac ccatggaagt ttgaatcatc tcctgcgcac taataccttc 1620
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gaactcaaca aacggcttca taaaaagg tctacaga ag agagacacct cctctatggg 1800
cgacctgcag tgctttatcg gactagatat gatatcttat atcacactga ctttgaagt 1860
ggttatagtg aaatattcct aatgccactc tggacatcat atactgtttc caaacaggct 1920
gaggtttcca gcgttcctga ccatctgacc agttgcgtcc ggctgatgt ccgtgtttct 1980
ccgagtttca gtgagaactg tttggcctac aaaaatgata agcagatgtc ctacggattc 2040
ctctttcctc cttatctgag ctcttcacca gaggctaaat atgatgcatt ccttgaacc 2100
aatatgggtc caatgtatcc tgctttcaaa cgggtctgga attatttcca aagggtattg 2160
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tatgactatg atggcttaca tgacacagaa gacaaaataa aacagtacgt ggaaggcagt 2280
tccattcctg ttccaactca ctactacagc atcatcacca gctgtctgga ttctactcag 2340
cctgccgaca agtgtgacgg ccctctctct gtgtcctcct tcctcctgcc tcaccggcct 2400
gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga' 2520
aagaccagcc gcagctaccc agaaatcctg aactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tccngactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcacttga gaagagggag agcaaggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcn tggnttctc tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc tgtagggcag gaaggccagc ccctcaaacy ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gcttnttggg gctcaaagg 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

27/292

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b -cells 3 (p65))
(RELA) gene.

<400> 43

```
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gtcccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctctctgggc a ccaaggacc 240
ctctcaccg gcctcaccac cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggtgagct ctgcccgac cgtgcaccc acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaaccct 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccagtgac agtgcgggac ccatcaggca ggccccctcg cctgccgcct gtcctttctc 540
atccccctt tgacaatcgt gcccacaaca ctgccgagct caagatctgc cgagtgaacc 600
gaaactctgg cagctgcctc ggtggggatg agatcttctt actgtgtgac aaggtgcaga 660
aagaggacat tgagggtgat ttcacgggac caggctggga ggcccaggc tccttttgcg 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac cctccctac gcagacccca 780
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ctcgcctagt gacagcccag agggcccccg acccagctcc tgcctccactg ggggcccccg 1560
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tgccttaata gtagggttaag ttgttaagag tgggggagag caggctggca gctctccagt 2340
caggaggcat agtttttagt gaacaatcaa agcacttga ctcttgcctt ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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aactctttcc tttggttggtg ctaagagggtg atgcccaagg tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctccctggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgtcatgg gaagaagcgc acgctgaagg ggtccattga gctctcccga 240
attcaaagtgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcggtng g 381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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attcagatat gtttgaacaa ttcttaaggc tacaaaacag aacatagaaa aataaacagg 120
aatatattca acacttacaa aaagtgtatg gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttaca gtaacatcac aaatgctcac 240
atcttcacat gctcttaaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
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aacttgattt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat ttttaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaata gtgtagccaa atatcattct cttcagctac cttaaagtaaa agacaaaaca 660
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gaacaacacg ctgcgagaat acagtctaca gtctgcatta aataagaa ta tatcagcatt 900
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caggtgagct ttggtcagtc tgttcttcaa aatatgtatg atcatatggg aatgaagttt 1200
cataatttcc aactcaaaaa tacaatgat cctcagttct atacttttgc ctctattctc 1260
ttataaagaa atatgtcaac ataacagtat gacataacag ttaaaaataag gacaaaagct 132 0
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tcaagcactt cttccatcat atcctagagg tgagatat gg gaaacagaaa gcaaatcagt 1560
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30/292

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```

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<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating
factor 1 (macrophage) (CSF1) gene.

<400> 48

```

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tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttcccatttt 360
aaaaatatgt gttttctag catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca gggtcact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating
factor 1 (macrophage) (CSF1) gene.

<400> 49

```
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gggggagggt ctgcactccc aaaccccagc gcagtgtcct ttccctgc tg ccgacagaac 120
ctggggctga gcaggttatc cctgtcagga gccctgggac tgggctgcat ctacgcccc 180
cctggcatgg tatccagctc ccatccactt cttcaccctt ctttctcct gaccttgggt 240
caacagtgat ggaccttcca actcttcacc caccctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagc 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage)
(CSF1) gene.

<400> 50

```
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caccagcgca gcgagcgagc gagcgagggc ggccgacgcg cccggccggg acccagctgc 120
ccgtatgacc gcgcccggcg ccgcccggcg ctgccctccc acgacatggc tgggctccct 180
gtgttgttg gtctgtctcc tggcgagcag gactatcacc gaggaggtgt cggagtactg 240
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cagagataac accccaatg ccatcgccat tgtgcagctg caggaactct ctttgaggct 480
gaagagctgc ttcaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
tgagacacct ctccagttgc tggagaaggc caagaatgtc tttaatgaaa caaagaatct 600
ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagctttg ctgaatgctc 660
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cagtgaacct gcctctgtct cccctcatca gcccctcgcc ccctccatgg ccctgtggc 780
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gctggtgccc agtgtcatcc tggctcttgc ggccgtcgga ggctcttg t tctacagggtg 1680
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```

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cccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
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tatcaatttg cactt 2475

```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```

atcngttgaa tagttgatcc catacatttc cagg tcctga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactggtcc ctggtaagtt tgtgtgtggt catcactctt tgagggatca nccgctcaga 180
gctgaggtac ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctgggt gatgtcctg ggatgagctt 360
ccttcagcca catcttccag ggnaggact ttnggcc 397

```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

```

ggacgaggca gggcggggcg gcgctctaag ggttctgctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagttt ccacctgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttcaa 360

```

37/292

gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttttttcnt ccaagtgaag gaagggattc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

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tggtatccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa
                                     3064

```

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 54

```

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tacttggtct tactattttt ttcctaacca tcaagagtgc ctcccaaat aa gnccagt 240
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ccaaacccta tttaccataa ttttcccggt cttttaagggt ttccatttgg aaacaaaaat 360
gtctatatgg ccggttggtg attancatgg ggnttttctt gggnttctct cttcccnct 420
ctttttaacc ggtgg
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```

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 55

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tggtgctgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
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<210> 56

<211> 10383

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(10383)

<223> adenomatosis polyposis coli (APC) gene.

<400> 56

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<210> 57
 <211> 404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(404)
 <223> 5' terminal sequence. mucin 1, transmembrane
 (MUC1) gene.

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<210> 58
 <211> 1721
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
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 <223> mucin 1, transmembrane (MUC1) gene.

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<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 59

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<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 60

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gtcgaccct cggaccgtgc ttccggacaa ctccccaga taccctgttg gcaagttctt 60
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gatgggccag caatcggaag tgagcaaat tgccgcaagt ntttcagccc ggcgncacca 300
ttccttgtag cttntntntt gaaccacgga gttttncttn aggtttccat tccngaaaa t 360
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<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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ttctgtttct ctccgtgctg ttctctcccg ctgtgcgctt gcccgctct cgctgtcctc 180
tctccccctc gccctctctt cggccccccc ctttcacgtt cactctgtct ctccactat 240
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ccgaaaagta caacatctgg cccgccccag cccgaagaca gccgctctc cctggacaat 360
cagacgaatt ctccccccc ccccaaaa aa aaaagccatc ccccgctct gcccgctgc 420
acattcgcc cccgcgactc ggccagagcg gcgctggcag aggagtgtcc ggcaggagg 480
ccaacgcccg ctgttcggtt tgcgacacgc agcaggaggg tggcgggcag cgctgcggc 540
ttccagacac caatgggaat cccaatgggg aagtcgatgc tgggtcttct cacttcttg 600
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gattggcttt aaacaccct cacaaccct ccccc 1356

<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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gcgtatgata ggcgtggag gggcacgctt agaaccatgc accaacaagg gcaggagaaa 120
acaaaatggt agccaggtgt tcttggtcat gccattgaat ttgggtctgt tctcagaaac 180
tctggaattg aagaagttgc aganaccgaa gataaaatgg tcgtttggag cagaaacacc 240
tgattttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

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gttctggggc tgggtgggga tccctcattt cccatgttaa gcttgaggaa gagatttcag 360
 ggtaggctcc ctgcagggaa actacttgtc cctcaacttt nggcctccca tagcatattt 420
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<210> 63

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(457)

<223> 5' terminal sequence. egf-like module
 containing, mucin-like, hormone receptor-like
 sequence 1 (EMR1) gene.

<400> 63

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 tgcantgatg gaggaaatca ggtgtttttt gntccaaacg gaccatttta ntcttctgtg 360
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<210> 64

<211> 3149

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3149)

<223> egf-like module containing, mucin-like,
 hormone receptor-like sequence 1 (EMR1) gene.

<400> 64

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 caaacacaaa gggtaataac tgtagagaca gtaccttggt c ccagcttat gccacctgca 180
 ccaatacggg ggacagttac tattgcactt gcaaacaagg cttcctgtcc agcaatgggc 240
 aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300
 cccagccctg tggctcctaac tcactctgca aaaacctgtc agggaggtac aagtgcagct 360
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

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<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. kiaa0427 gene product
(KIAA0427) gene.

<400> 65

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atcccgtgga ggggtggcggg gctcctggcc tcgtctgggt gaggttgga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaagcca ccaggccttg gggagcaggg ctttggaag 240
caggccgcct cgga gaaaaa caatgactaa ctcatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

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ccccggggcn aggggngaaa gcaattncaa agcctttagg aaatttcaat tt 412

<210> 66

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 5' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 66

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tatggaagga aaacgttaag actatttttt ttttaaagaa acaacagtca agcctaaaat 120
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gaaggccgcy tccgagttga cctctgaatg tatgtgatga gaggcagagc tgggatattg 300
catttcttaa ggggtgcatt gcttttcccc ttccgcccgc ttctttggcg catggaagga 360
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gggatngagt tagttcattt tt 442

<210> 67

<211> 5737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5737)

<223> k1aa0427 gene product (K1AA0427) gene.

<400> 67

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<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase (SYK) gene.

<400> 68

```

tctttctttc ttctcttaac tggctacatg cttagaaact gcactggtca aacttgattt 60
tctttttaaa gcctcaaaac atttttattg tcaggaaagc ttttcagtgg ccagggatca 120
gtctcatggc cgtagaagca gccaaattcc tctgcctttg ctttcccttc aggagtca ca 180
tgctaaggca tccttggggc atttgggaaa agngccgctt gggggtgaga gtgctctagg 240
gccactctgc aatgtccctg gggncgatg aggtaacaaa tgcaccccg ggaccagag 300
gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377

```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase (SYK) gene.

<400> 69

```

ttaattttgg aggccttcca caacttcag gttcccatcc tgcgacttgg tcagcgggtg 60
gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgccaagga gaaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaaact 180
tgcacccggg gcttgcagga caaagggccc cca gaggagg aagccctacc cntgggacac 240

```

50/292

agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

gaggaagagc cgcggggccc ggggctgagg ccaccccggc ggggctgga gagcgaggag 60
gagcgggttg ccccgcgctg cggccgcctt cgcctcacct ggcgcagggtg g acacctgcg 120
cagggtgtgt cctccggcc cctgaagcat ggccagcagc ggcattggctg acagcgccaa 180
ccacctgccc ttctttttcg gcaacatcac ccgggaggag gcagaagatt acctgggtcca 240
ggggggcatg agtgatgggc tttatttget gcgccagagc cgcaactacc tgggtggctt 300
cgccctgtcc gtggcccacg ggaggaaggc acaccactac accatcgagc gggagctgaa 360
tgccacctac gccatcgccg gtggcaggac ccatgccagc cccgccgacc tctgccacta 420
ccactcccag gagtctgatg gcctggcttg cctcctcaag aagcccttca accggcccca 480
aggggtgcag cccaagactg ggccttttga ggatttgaag gaaaacctca tcagggaata 540
tgtgaagcag acatggaacc tgcagggtca ggctctggag caggccatca tcagtacaga 600
gcctcagctg gagaagctga tcgctaccac agcccatgaa aaaaatgcctt ggttccatgg 660
aaaaatctct cgggaagaat ctgagcaaat tgccttgata ggatcaaaga caaatggaaa 720
gttctgtatc cgagcgagag acaacaacgg ctctacgccc ctgtgcctgc tgcacgaagg 780
gaaggtgtcg cactatcgca tcgacaaaga caagacaggg aagctctcca tccccgaggg 840
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ccccgaggag atcaggccca aggaggtta cctggaccga aagctgctga cgctggaaga 1200
caaagaactg ggctcttgga attttggaa tgtagaaaag ggctactacc aaatgaaaaa 1260
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gatgatcggg atatgcgagg ccgagtcctg gatgctggtt a tggagatgg cagaacttgg 1440
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ggttcatcag gtttccatgg gcatgaagta cttggaggag agcaattttg tgcacagaga 1560
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agggatgaaa ggaagtgaag tcaccgctat gtagagaaa ggagagcgga tgggg tgccc 1860
tgcagggtgt ccaagagaga tgtacgatct catgaatctg tgctggacat acgatgtgga 1920
aaacaggccc ggattcgcag cagtggaaact gggctgcgc aattactact atgacgtggg 1980
gaactaacg ctcgccgacc tgcgttggtg tgcctttgat cacaggagca atcacaggaa 2040
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agcaaaggca gtccggggag aaaagacgga tggcaggatc caaggggcta gctggatttg 2220
tttgttttct tgtctgtgtg attttcatac aggttatttt tacgatctgt ttccaaatcc 2280
ctttcatgtc tttccacttc tctgggtccc ggggtgcatt tgttactcat cgggcccagg 2340
gacattgcag agtggcctag agcactctca cccaagcgg ctttttcaa atgcccagg 2400
atgccttagc atgtgactcc tgaagggaag gcaaggcag aggaatttgg ctgcttctac 2460
gtccatgaga ctgatccctg gccactgaaa agctttcctg aca ataaaaa tgttttgagg 2520
ctttaaaaag aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaattgtga gtttcaatcc tgaaagtttc 60
ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaagggttt 120
ctgcaagata cgtttcctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
ggagattcat ccctcacatg cctgggctng ggaatgttca gtgcatgtga cgccctatt 300
tttctccttt t 312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctaggtaca acttttggca tgggt tttttc 60
tttacttcaa gtggtttctg gagaaagtgg ctatgtctaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
ttcactgacc tgtgcttttg aggaccaga tgtcaacacc accaatctgg aatttgaaat 240
atgtggggcc ctgctggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgaga 360
aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggctccttt 420
tgacctgagt gtcattctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc 480
acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa 540
ggatgaaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tcctgcagag 600
aaagctccaa cgggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt 660
taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
tagctcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt 780
cgctctgttg gtcattcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtagt 840
gccagtcctc ccgcatcata agaagactct ggaacatctt tgtaagaaac caagaaaaaa 900
tttaaagtgt agtttcaatc ctgaaagttt c ctggactgc cagattcata ggttgatga 960
cattcaagct agagatgaag ttggaagttt tctgcaagat acgttctc agcaactaga 1020
agaatctgag aagcagagggc ttggagggga tgtgcagagc cccaactgcc catctgagga 1080
tgtagtctgc actccagaaa gctttggaag agattcatcc ctacatgcc tggctgggaa 1140
tgtcagtgca tgtgacgccc ctattctctc ctcttcagg tccctagact gcaggagag 1200
tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttggga ctacaaacag 1260
cacgctgccc cctccatttt ctctccaatc tggaaatcctg acattgaacc cagttgctca 1320

52/292

```

gggtcagccc attcttactt ccctgggatc aaatcaagaa gaagca tatg tcaccatgtc 1380
cagcttctac caaaaccagt gaagtgtgtaag aaaccagac tgaacttacc gtgagcgaca 1440
aagatgattt aaaaggggaag tctagagtgc ctagtctccc tcacagcaca gagaagacaa 1500
aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
gtcacaaggt ttaaggtgac ccaatgattc agctattt 1658

```

<210> 73

<211> 236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(236)

<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73

```

taaaaacaat agaaaaaaat caactttaaa aagcaaaatg tacttaaata aaaaaatta 60
gggttttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt tttattaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaatct taaaattttt taaaanccaa ttcttaaata ccaaatctgt taaggg 236

```

<210> 74

<211> 413

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(413)

<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74

```

acgtctccac acatcagcac aactacgcag cgcctccctc cactcggaag gactatcctg 60
ctgccaaagag ggtcaagttg gacagtgtca gagtcctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccggagt tgggaaaaca atgaaaaggc ccccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggagggagcc aaaagtcat tttnttgaag 360
gagggntttt ttttccgggn aacgacgagg aaccattttn aacacaant ttt 413

```

<210> 75

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

```
ctgctcgagg cgcaccgc cgggccccgg cgtccctgg ctccccctct gctcgagaa 60
gggcagggct tctcagaggc ttggcgaggaa aaaagaacg g agggagggat cgcgctgagt 120
ataaaagccg gttttcgagg ctttatctaa ctgctgtag taattccagc gagaggcaga 180
gggagcgagc gggcgggcgg ctaggggtga agagccgggc gagcagagct gcgctcgagg 240
cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctcccg 300
cttgatcccc caggcca gcg gtccgcaacc cttgccgat ccacgaaact ttgcccatag 360
cagcgggcgg gcactttgca ctggaactta caacaccgca gcaaggagcg gactctcccg 420
acgcggggag gctattctgc ccatttgggg acaattcccc gccgctgcca ggaccgctt 480
ctctgaaagg ctctccttgc agctgcttag acgctggatt ttttcgggt agtggaac c 540
cagcagcctc cgcgacgat gcccctcaac gttagcttca ccaacaggaa ctatgacctc 600
gactacgact cgggtcagcc gtatttctac tgcgacgagg aggagaactt ctaccagcag 660
cagcagcaga gcgagctgca gccccggcg ccagcgagg atatctgga gaaattcgag 720
ctgctgcca ccccgccct gtcccctagc cgcgct ccg ggtctgctc gccctctac 780
gttgcggtca cacccttctc ctttcgggga gacaacgagc gcggtggcgg gagcttctcc 840
acggccgacc agctggagat ggtgaccgag ctgctgggag gagacatggt gaaccagagt 900
ttcatctgcy acccgacga cgagacctc atcaaaaaca tcatcatcca ggactgtatg 960
tggagcggtc tctcg gccgc gcccaagctc gtctcagaga agctggcctc ctaccaggct 1020
gcgcgcaaag acagcggcag cccgaacccc gcccgcgccc acagcgtctg ctccacctcc 1080
agcttgatcc tgcaggatct gagcgccgcc gcctcagagt gcatcgacct ctcggtgggc 1140
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gccttctctc cgtcctcgga ttctctgctc tctcagcgg agtccctccc gcagggcagc 1260
cccagacccc tgggtgctca tgaggagaca cgcgccacca ccagcagcga ctctgaggag 1320
gaacaagaag atgaggaaga aatcgatgtt gtttctgttg aaaagaggca ggctcctggc 1380
aaaaggtcag agtctggatc acctctgtc t ggaggccaca gaaaacctcc tcacagccca 1440
ctggtcctca agagggtgcca cgtctccaca catcagcaca actacgcagc gcctccctcc 1500
actcggaagg actatcctgc tgccaagagg gtcaagttgg acagtgtcag agtccctgaga 1560
cagatcagca acaaccgaaa atgcaccagc ccaggtcct cggacaccga ggagaatgtc 1620
aagaggcgaa cacacaacgt cttggagcgc cagaggagga acgagctaaa acggagcttt 1680
tttgccctgc gtgaccagat cccggagtgt gaaaacaatg aaaaggcccc caaggtagtt 1740
atccttaaaa aagccacagc atacatcctg tccgtccaag cagaggagca aaagctcatt 1800
tctgaagagg acttggttgc gaaacgacga gaacagttga aa cacaaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg tttcaaatgc atgatcaaat gcaacctcac aaccttggct 1980
gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaatgg actttgggca 2040
taaaagaact tttttatgct taccatcttt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
```

<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

54/292

<400> 76

```
tcacagcact agagaccctg ttaaataagg gatatgagtc agaattggctt attcacagat 60
gggggccaga ttcagtgggtt ggaacacaga caccacagtg agctcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgtcctctg aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggtcttt                                     260
```

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 77

```
cattctggtt catagatggc atcttttcac tgtgttctca cattggtgga aaggaagaac 60
tctggtttct tcacttcctt ataagggcac caatcttatt cacgagggtc tcaccctcga 120
aataatcacg tcctcaaaac ccccaccttc taatattcta ataccatcac gtgagggcctt 180
aggtttcaac ataagaattc ggtggtggtn gggttngggg gagagggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaadc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctncgttt taaccggggc cgcctttttc caggacacat 360
gttccttccc tggnggccac atnttgncc ttnaggccan tccagggca 409
```

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

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tccagcctt cccatcccc caccgaaagc aaatcattca acgacccccg accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgccttccc tccccgcgcg ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggtg acggcggacc agccgcgctg 180
ggtgagccac caccaccccg ccgtgctcaa cgggcagcac ccggacacgc accacccggg 240
cctcagccac tcctacatgg acgcggcgca gtacccgctg ccggaggagg tggatgtgct 300
ttttaacatc gacggtcaag gcaaccacgt cccgccctac ta cggaaact cggtcagggc 360
cacggtgcag aggtaccctc cgaccacca cgggagccag gtgtgccgc cgcctctgct 420
tcattgatcc ctaccctggc tggacggcgc caaagccctg ggcagccacc acaccgcctc 480
ccccgtgaat ctacgcccct tctccaagac gtccatccac cagggctccc cggggccctc 540
ctcgcgtctc ccccgggcct cgtcctctct cttgtcgggg ggccacgcca gcccgacct 600
cttcacctc cgcgccacct cgccgaagga cgtctcccc gaccatcgc tgtccacctc 660
aggtcgcggc ggctcggccc ggcaggacga gaaagagtgc ctcaagtacc aggtgcccct 720
gcccagacag atgaagctgg agtcgtccca ctcccgtggc agcatgaccg ccctgggtgg 78 0
agcctcctcg tcgaccacac acccatcac cactacccg ccctacgtgc ccgagtacag 840
ctccggactc tccccccca gcagcctgct gggcggtcc cccaccggct tcggatgcaa 900
```

```

gtccaggccc aaggcccgt ccagcacagg caggagtggt gtgaactgtg gggcaacctc 960
gacccactg tggcgcgag atggcacggg acactacctg tgcaacgcct gcgggtcta 1020
tcacaaaatg aacggacaga accggccct cattaagccc aagcgaaggc tgtctgcagc 1080
caggagagca gggacgtcct gtgcgaactg tcagaccacc acaaccacac tctggaggag 1140
gaatgccaat ggggacctg tctgcaatgc ctgtgggctc tactacaagc ttcaaatat 1200
taacagaccc ctgac tatga agaaggaagg catccagacc agaaaccgaa aaatgtctag 1260
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acagggcccc cagcgagagt ccctgcagtc cctttcgact tgcatTTTTT caggagcagt 1560
atcatgaagc ctaaacgcga tggatatatg tttttgaagg cagaaagcaa aattatgttt 1620
gccactttgc aaaggagctc actgtggtg t ctgtgttcca accactgaat ctggaccca 1680
tctgtgaata agccattctg actcataatc cctatttaac agggctcta gtgctgtgaa 1740
aaaaaaaaat cctgaacatt gcatataact tatattgtaa gaaatactgt acaatgactt 1800
tattgcatct gggtagctgt aaggcatgaa ggatgccaa aagttaagg aatatgggag 1860
aaatagtgtg gaaattaaga agaaactagg tctgatatc aaatggaca actgccagtt 1920
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aagagaaaag aaaaaaaaag aaaaaagttg taggcgaatc atttgtcaa agctgttggc 2040
cctctgcaaa ggaaatacca gttctgggca atcagtgtta cc gttacca gttgccattg 2100
agggtttcag agagcctttt tctaggccta catgctttgt gaacaagtcc ctgtaattgt 2160
tgtttgtatg tataattcaa agcaccaaaa taagaaaaga ttagatttta ttcatcata 2220
ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgtttctt 2280
tcgtttgttt gtttcaa tat tttccttctc totcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaa aaaa 2365

```

<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

```

ttgtatnttt naaataatct ttattgtcac tagtataaaa cagagcagat caactggcct 60
ctcggctctgt acaagtgtg gggcgtgaaa ccgctgggct gcccactt ctccataat 120
tccctgccct agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtgggg ctgttttcta tctgaggag 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgcccc 300
tgtggccgat ccnaggtcc actnggat 328

```

<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

```
ggctccccac ccttgagaag tgcctcagat aataccctgg tggccatgga cttctctggc 60
catgctgggc gtgtcattga gaacccccgg gaggtcttga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctcagcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggct tngtagacgg cctgttcctg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatttt aagcattggg 42 0
tgattggc 428
```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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tgtagagaag cgggagtgga tctgaaataa aatccaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgtctggg ctctccagg acaaggga c 180
acaactgggt cggtaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tctgggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccaccg gcaggaacct tcgagaggag gagaggc gtg ccacctccct cccctctatc 420
cccaaccctt tccctgagct ctgcagtcct ccctcacaga gcccaattct cgggggcccc 480
tccagtgcaa gggggctgct cccccgcgat gccagccgcc cccatgtagt aaaggtgtac 540
agtgaagtgc gggcctgcag gtctgtggag gtggcagcag gtgccacagc tcgccacgtg 600
tgtgaaatgc tgggtcagcg agctcacgcc ttgagcgacg agacctggg gctgggtggag 660
tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtccgt ggtggaagtg 720
caggctgcct ggcccgtggg cggagatagc cgcttcgtct tccgaaaaa cttcgccaag 780
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cgctttttct gtttcttgcg ccgatctggc ctctattact ccaccaaggg cacctctaag 1020
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acgcgggtgg ccctctgacc aggcgtgga ctggctcatg cctcagccc ccttcaggct 1860
gcccgcgcgc cctccacca tccagtggac tctggggcgc ggccacaggg gacgggatga 1 920
```

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ggagcgggag ggttccgcca ctccagtttt ctctctgct tctttgcctc cctcagatag 1980
 aaaacagccc ccactccagt ccactcctga cccctctcct caagggaagg ccttgggtgg 2040
 cccctctcc ttctcctagc tctggaggtg ctgctctagg gcagggaatt atgggagaag 2100
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<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
 beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
 acagacagat aaagttccaa gtaaaacggg agctgctaaa aagggtatgt acttataatt 120
 gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
 actatttgca tttttttatc ataaaacaat taaggaaagta taagtgttta taaggaggac 240
 ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300
 gttgtanttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
 gene.

<400> 83

atggccaagt cgggtggctg cggcgcgagg gccggcggtg gcggcgggcaa cggggcactg 60
 acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccaaaca aaatgattct 120
 tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
 ctctcgtcctg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
 gatgaagatg taggaatgaa ttgcaggag gttacctttg tgccaggttt atacaagatc 300
 tttgatgaaa ttttggttaa tgcgtctgac aataaacaga gggataagaa catgacttgt 360
 attaaagttt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
 attccagtag tagaacacaa ggtagagaaa gtttat gtcc ctgctttaat tttggacag 480
 cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacagggtg tcgtaatggg 540
 tatggtgcaa aactttgtaa tattttcagt acaaagtta cagtagaac agcttgcaa 600
 gaatacaaac acagttttta gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
 aaaattaaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
 aaatttaaga tggaaaaact tgacaaggat attgtggccc tcatgactag aaggccatat 780
 gatttggtgct gtctgtgtag aggggtcaag gtcatgttta atggaaagaa attgcctgta 840
 aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
 gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

gaaaaaggat tccagcaaat cagctttgta aatagtattg caactacaaa aggtggacgg 1020
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 aattgcctta ttgaaaatcc aacttttgat tctcagacta aggaaaaacat gactctgcag 1200
 cccaaaagtt ttgggtctaa atgccagctg tcagaaaaat tttttaagc agcctctaata 1260
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 ccactcaggg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaat 1560
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 gaccagtgaa aagcctggaa agaagcaca gaaaaggcag cagaagagga tgaacacaa 3360
 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaga ttttaattat 3420
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 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaatctca agaacgagaa 3600
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 gatgatgaca ataattgatt agaggattt aaagttaaag catctcccac aacaaatgat 4200
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 ggcaaatcaa aagccactcc agaaaaatct ttgcatgaca aaaaaagtca ggattttgga 4320
 aatctcttct catttcttcc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacggg agctgctaaa aagggaaaac cgtcttcaga tacagtccct 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaaactc tgactcggat 4560
 tcagaatttg gcattccaaa gaagactaca acaccaaaag gtaaaaggccg aggggcaag 4620

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```

aaaaggaaag catctggctc tgaaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttcctac tgagccacct tctctgccac gaaccggtcg g gctaggaaa 4800
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa                                           4866

```

<210> 84
 <211> 311
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(311)
 <223> 3' terminal sequence. caspase 4,
 apoptosis-related cysteine protease (CASP4) gene.

```

<400> 84
cactttttatt gaaatacaaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggtcg gg ctgcttgt ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatata ttgtcatgga cagtcgttct atgggtggca tttgagcttt ggccttgga 180
gtttcaaatg attgctgtac cttccgaaat acttctcta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t                                           311

```

<210> 85
 <211> 1291
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1291)
 <223> caspase 4, apoptosis-related cysteine
 protease (CASP4) gene.

```

<400> 85
gctctttcca acgctgtaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggt ttggaatccc tgggcaaaga tttcctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaattctaca gatgccctca 360
agctttgtcc tcatgaagaa ttcttgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaacaaac cgcacacgcc tggctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggtctgga ctatagtgtg gatgtagaag agaattctgac agccagggat atggagtcag 600
cgctgagggc atttgctacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gagggaatct gcggaactgt gcatgatgag aaaaaaccag 720
atgtgctgct ttatgacacc atcttcaga tattcaacaa ccgcaactgc ctgagctctga 780
aggacaaacc caaggatcatc attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctcttc acagtcactc gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgtttc tgctcttcaa 960

```

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```

cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttgggtg ct gccacctaga ggaagtattt cggaaggtag 1080
agcaatcatt tgaaactcca agggccaaag ctcaaatgcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291

```

<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 86

```

tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttggagg ctttttttgc agttggccac aggggcgttg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaacn ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctctt gatgcaggcg aagaacttgg cctggnccc gttnatgttc 240
ttctctgtga cccagtccat ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319

```

<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 87

```

cgcagcaaac acatccgtag aaggcagcgc ggccgcga g agccgcagcg ccgctcgccc 60
gccgcccccc acccgccgc cccgccgcgc gaattgcgc ccgcgccct cccctcgcg 120
ccccgagaca aagaggagag aaagtattgc cggccgagcg gggcaggtga ggagggtgag 180
ccgcgcggga ggggccgcgc tcggcccccg ctcagcccc gcccgcgccc ccagcccgc 240
gccgcgagca gcgcccgc ac cccccagcgc cggccccgc ccgccagcc ccccgcccc 300
ccatgggcgc cgcggccgc accctgcgc tggegtcgc cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgc tcagctgct ccccggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgc tcagtgaag ggaagtggac tctggaacg 480
acatttatgg caaccctatc aagaggatcc agtatgat caagcagata aagatgttca 540
aagggcctga gaagatatata gagtttatc acacggcccc ctcctcgga gtgtgtggg 600
tctcgctgga cggtggagga aagaaggaat atctcattgc aggaaggcc gagggggag 660
gcaagatgca catcacctc tgtgacttca tcgtgcc tg ggacaccctg agcaccacc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgtacatc tcctccccgc acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900

```

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cctgtgcgtg gtaccgcggc gcggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctggtccagc tctgacatcc cttcctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta tttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcag gcgggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180
ccaatcataa aaaagtcag accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacaag aatttgccc ccaaccgagt gcccgcggn tgngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120
tacggccggg cctggccatg gcgctgagcg ggteccaccga gccctgcgcg cagtgttcca 180
tctcctccat cggcgtagtg gggcaccgcg agggacaacc gcagccacag cgcccatbbc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90

```
gatcccggtg ccagggaccc tgcccagttc caggcgtcgc ctaaccacaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgcacg gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg 240
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagt ggcaccgagg aggacaaccg cagccacagc 360
gcccaattct ttgagtttct caccaaggag ctagccctgg gcc aggaccg gatacttatt 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggtcat gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgaggcctg gagataacca gctttggatt atcccgcatg caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag cttcctcatt 660
caaaaa
```

<210> 91

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91

```
gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaacggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttggtg atgattcggg 180
catttcaggg agcttgagga taattgtcga ttttatgtga atccctgcgt aggcaatggg 240
agaggttata ataaggcagg aaagggcgag actcttcac agccatctgc aggggatggg 300
aagtccccga ccagacaggg gtagatctca ttttctttgg gtttccagg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt
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<210> 92

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(243)

<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92

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gaagaatcgg aacatacagg ctttgatcgc aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctccc tgctgctgct ggggtgttcaa 180
acctgctect gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat
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<210> 93
 <211> 833
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(833)
 <223> prolactin (PRL) gene.

<400> 93
 aaacatgaac atcaaaggat cgccatggaa aggggtccctc ctgctgctgc tgggtgtcaaa 60
 cctgctgctg tgccagagcg tggccccctt gcccctctgt cccggcgggg ctgcccgatg 12 0
 ccaggtgacc cttcgagacc tgtttgaccg cgccgctgctc ctgtcccaact acatccataa 180
 cctctctca gaaatgttca gcgaattcga taaacgggtat acccatggcc gggggttcat 240
 taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaaag acaaggagca 300
 agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgatcctg 360
 gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgagggc 420
 tatctatcc aaagctgtag agattgagga gcaaaccaaa cggcttctag agggcatgga 480
 gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
 gggacttcca tccctgcaga tggctgatga agagtctcgc ctttctgctt attataacct 600
 gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tctgaagtg 660
 ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720
 tccctaataa tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
 tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94
 <211> 304
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(304)
 <223> 3' terminal sequence. prolactin receptor
 (PRLR) gene.

<400> 94
 actaagcagt gtgcttttat ttcatgtaac acatagtttt ataactaaca gcaaaaagta 60
 aatctacaaa tcacagttag gaaacataat gatttggtct ggaatcagct gctggagaaa 120
 gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gctttagtag tgcagtcctg 180
 actacattct tgaggcattt cacgtactct gtagtggtac ctgaagaaaa atcacatttt 240
 aaccaatcat tcattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
 cggg 304

<210> 95
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 95
gaggtcattg agaagccaga gaatcctgaa acancccaca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaatgttc aacatggccc 120
ttaccacagc ccagccagca caaccccaga tcctcttacc acaatattac tgatgtgtgt 180
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgncctgg gttgcttgcc 360
ccaggg 366

<210> 96
<211> 2723
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2723)
<223> prolactin receptor (PRLR) gene.

<400> 96
ggaggctgaa atcccagac gccggttttc tgggctgggc tttctgctta ctactcctt 60
ctccctcttt ctggatttta ccgaccgttc gcgaaacagc tttccacaca atggagcttc 120
atgtcctcgt gcaggaagta ctcacgcact gatgtggcag actttgctcc ctgacaaaac 180
taaagaactc tcctattcat ggaggcgaac actgaggatg ctttccacat gaaccctgaa 240
gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
catctgcaac cgttttctact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
tacctcctgg aaaacctgag atctttaaat gtggttctcc caataaggaa acattcacct 420
gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
gggaaggaga gacactcatg catgaatgac cagactacat aaccggtggc cccaactcct 540
gccacttttg caagcagtac acctccatgt ggaggacata catcatgatg gtcaatgcc 600
ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagtgc 660
agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720
acctgtggat taaatggtct ccacctaccc tgattgactt aaaaactggt tgggtcac gc 780
tcctgtatga aattcgatta aaacccgaga aagcagctga gtgggagatc cattttgctg 840
ggcagcaaac agagttaag attctcagcc tacatccagg acagaaatac cttgtccagg 900
ttcgtgcaa accagacctg ggatactgga gtgcatggag tccagcgacc ttcattcaga 960
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gcatctttcc gccagttcct gggccaaaaa taaaaggatt tgatgctcat ctgttgaga 1140
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acactgactc aggcgggggg agctgtgaca gcccttcctt tttgtctgaa aagtgtgagg 1380
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agtctagaga agaggggaaag gcaacccagc agagggagggt agaaagcttc cattctgaga 1740
ctgaccagga tacgccctgg ctgctgcccc aggagaaaac cccctttggc tccgctaaac 1800
ccttgagatta tgtggagatt cacaaggtca acaagatgg tgcattatca ttgctaccaa 186 0

65/292

```

aacagagaga gaacagcggc aagcccaaga agcccgggac tcctgagaac aataaggagt 1920
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ctaaaaacgt ggcttgcttt gaagaatcag ccaaagaggc cccaccatca cttgaacaga 2040
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tgggtgggtt ggattacctg gatcccgcat gttttacaca ctctttcac tgatagcttg 2160
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aatgctcaag aatgtagtca gactgacact actaaagctc ccagctcctt tcatgctcca 2280
tttttaacca ct tgcctctt tctccagcag ctgattccag aacaaatcat tatgtttcct 2340
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gctttcatga tttggcatgg gacagacgga aatgaaattg tcaaaattgt t taccataga 2520
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aactgcataa cctttacact cctcgtccat tttattagga ttaccctaat ataaccattt 2640
aaagaaagaa tgcattccag aacaaattgt ttacataagt tcctatacct tactgacaca 2700
ttgctgatat gcaagtaaga aat                                     2723

```

<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

```

gtacagttac cttttattta tagcgaaaat gggttttttc atttacagag taacaaagat 60
ttttctttaa ataatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctcca 240
aagtggggga agggcaaata caatttcnt ttgggggggg ataggngac cccctttgca 300
gagaggggtt aggtgggggt tccccccggn acacacaggc aagggtttgg gngccccttg 360
tgggg                                           365

```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

```

nattcggcac tagggggcac ctgaccacac gccccacag gctctgacca gcagcctatg 60
aggggggttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttg 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttg gttcccaata caaaaatacc tactgctgag agggngtget gaccattttg 300

```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc cttttttttn aggttttntt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

gcagccagag ctcagcaggg ccctggagag atggccacgg tcccagcacc ggggagg act 60
ggagagcgcg cgctgccacc gcccctatgtc tcagccaggg cttccttcct cggctccacc 120
ctgtggatgt aatggcggcc cctgctctgt cctggcgtct gccctcctc atcctcctcc 180
tgccctggc tacctcttg gcactctcag cggatgaatg cacttcccag ttcacatgct 240
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tcccgtgag tcaagcatcc tgggcctgca acctgacct cggagcccca gattctcaga 420
aactgaccac agttgacatc gtcaccctga ggggtgctgt ccgtgagggg gtgcgatgga 480
gggtgatggc caccaggac ttcaagccct ttgagaacct tcgcctgatg gcccctatct 540
ccctccaagt tgtccactg gagaccaca gatgcaacat aagctgggaa atctcccaag 600
cctccacta ctttgaaga cactggagt tcgagggccg gacgtgtcc ccaggccaca 660
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aatctgccag aaacttctag cgtcagtgct ggaggagaa gctgtcagg acccagggcg 2580

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cctggagaaa gaggccctgt tactattcct ttgggatctc tgaggcctca gagtgccttg 2640
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cctgctgcat cttcccacag tggcttcaca gaccacaaag agaagctgat ggggagtaaa 2760
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ttccttaata ttttttcttt aagtcagttc attttcgtt aaatacattt ataaagaaaa 3960
atctttgtta ctctgtaaat gaaaaaaccc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat 4034

```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 100

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aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaaactt cttggcatcc ttcatgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggtccctt tgccaaagggt ggggccaac ataattttgg cttttctggc cttcaaaaa 420
catatttccn tcgcgttttg gggg 444

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<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
 <222> (1)..(396)
 <223> 5' terminal sequence. gata -binding protein 3
 (GATA3) gene.

<400> 101
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 acccctgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctagcaaadc 120
 caaaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctctgttaac 180
 ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
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 ccacaccacc cctccagctg ggtcaccgcc ntgggttttag agccttgctn gatggttcac 360
 agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
 <211> 416
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(416)
 <223> 5' terminal sequence. placental growth
 factor, vascular endothelial growth factor -related
 protein (PGF) gene.

<400> 102
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 acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccct tggaggagag 120
 agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgtctggt 180
 acctgccctc tattttattag ccaactgttt ccctgtgaa tgcctcgctc cttcaagac 240
 gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gaaaaag 300
 agagaagcca gccacagacc cctggggagc ttccgcgtt tgaaagaagc aagacaagtt 360
 ggccttggtt aggggcaagg ttagggccca ggaggccctn gggaagtttt tcaggg 416

<210> 103
 <211> 1645
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1645)
 <223> placental growth factor, vascular
 endothelial growth factor -related protein (PGF)
 gene.

<400> 103
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 tccccgggac ccgctgccc ctggcgccc cgccccgcc ggccgctccc cgtcgggttc 120
 ccagccaca gccttaccta cgggctcctg actccgcaag gcttcagaa gatgctcgaa 180
 ccaccggcgg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240
 ctctctctgt gccaggggct ccccggggga tgagcatggt ggttttcct cggagcccc 300

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```

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ggctcgtcag aggtggaagt ggtacccttc caggaagtgt gggcccgag ctactgccgg 480
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tttcggccg aggtgccacc accctgccc cactaagaga cacatacaga gtgggccccg 1440
ggctggagaa agagctgcct ggatgagaaa cagctcagcc agtggggatg aggtcaccag 1500
gggaggagcc tgtgcgtccc agctgaaggc agtggcaggg gagcagggtc cccaagggcc 1560
ctggcaccac cacaagctgt ccctgcaggg ccatctga ct gccaaagccag attctcttga 1620
ataaagtatt ctagtgtgga aacgc 1645

```

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein
ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

```

ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aagggtcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309

```

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

```

atggagaagc tgcaccagtg ttattggaaa tcaggagaac ctcaagtctga cgacattgaa 60
gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
actgagggct gtggaaatga agcctgcacg aatgagtttt gtgcttctctg tccaactttt 180
cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
aaactctgtg atcctcatcc ctccaagaaa ggagcaagct cagcttacct tgagaactcg 300
aaaggtgccc ccaacaactc ctgctctgag ataaaaatga aca agaaagg cgctagaatt 360
gatttttaag atgtgactta cttaacagaa gagaaggat atgaaattct tgaattatgt 420
agagaaagag aggtattatc ccctttaatc cgtgttattg gaagagtttt ttctagtgtc 480
gaggcattgg tacagaagctt ccggaaaagt aaacaacaca ccaaggaaga actgaaatct 540
cttcaagcaa aagatgaaga c aaagatgaa gatgaaaagg aaaaagctgc atgttctgct 600
gctgctatgg aagaagactc agaagcatct tcctcaagga taggtgatag ctcacaggga 660
gacaacaatt tgcaaaaatt aggccctgat gatgtgtctg tggatattga tgccattaga 720
agggctctaca ccagattgct ctctaatagaa aaaattgaaa ctgcctttct caatgcactt 780
gtatatttgt cacctaactg ggaatgtgac ttgacgtatc acaatgtata ctctcgagat 840
cctaattatc tgaatttgtt cattatcgga atggagaata gaaatctcca cagtctgaa 900
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caaggaaaac tgatcagact gtggtctaaa tacaatgcag a ccagattcg gagaatgatg 1020
gagacatttc agcaacttat tacttataaa gtcataagca atgaatttaa cagtcgaaat 1080
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ccctttatat tgaatgctgt cacaagaat ttgggattat attatgaca tagaattcgc 1500
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ggaagccgga atctagat tt ccaagcacta gaagaaacta cagaatatga cggtaggtat 2340
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cagaaaagac tcttcttgca gtttacaacg ggcacagaca gagcacctgt gggaggacta 2460
ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaagggt acctaca tct 2520
catacttgct ttaatgtgct ttacttccg gaatactcaa gcaaagaaaa acttaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttgga tgctgtaa 2628

```

<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220> -

<221> misc_feature

<222> (1)..(363)

71/292

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106
aattttaatt ctagcacctg aagctataca agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagncgg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
gggggngggg ttcttgaggt aggttatggt ggact gggnc caaggntggg ggggtaccacc 360
cag 363

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgctgtgtg atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatattc ta tgtgggtcaaa tatttggact 180
catttaggac ttagatattt cagtgtactt gattttttta tttactcct tttcacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgtttttgtt tgtaataata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgntt 408

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108
atggccgcgg cggctggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcccgg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgtaacg 120
gattatgac caaccattga agattcttac acaaaagcagt gtgtgataga tgacagagca 180
gcccggctag atatttttga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg ctctctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctacagagtaa aggatcgtga tgagttccca 360
atgattttta ttggtataaa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc ctccaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600

gtcattttct ag

6 12

<210> 109

<211> 592

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(592)

<223> 5' terminal sequence. tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE) gene.

<400> 109

```
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgatgt ctggctcctt ggagtccttc tttgggagat 180
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagtg ctggcgggac cgctccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnctgagctg ccatccagcc 480
agaactnggt ctgttgccg gagcaaatTT ggtgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592
```

<210> 110

<211> 3845

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3845)

<223> tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE) gene.

<400> 110

```
cgctcgtcct ggctggcctg ggtcggcctc tggagtatgg tctggcgggt gccccctttc 60
ttgctcccca tctctttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggctcgga cgctggggc cc gccccctgc tgctggagaa ggacgaccgt 240
atcgtgcgca ccccgcccgg gccacccctg cgctggcgc gcaacggttc gcaccaggtc 300
acgcttcgcg gcttctccaa gccctcgga ctcgtggcg tcttctctg cgtgggcggg 360
gctggggcgc ggcgacgcgc cgctcatctac gtgcacaaca gccctggagc ccacctgctt 420
ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacaccctg 540
gactggcatg aagcccagga tgggcgggtc ctgctgcagc tcccaaatgt gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc cctgggcag cg ccttcttt 660
cggtcatcgt tgcggggttg tggggctggg cgctgggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcaact gcacccgctg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840
```

```

caggagcagt gccagggcat atcaggctgc cggggcctca ccttctgcct cccagacccc 900
tatggctgct cttgtggatc tggctggaga ggaagccagt gccaagaagc ttgtgcccc 960
ggtcattttg gggctgattg ccgactccag tgccagtgtc agaatggtgg cacttgtgac 1020
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aagccagacg gcactgtgct cctgtccacc aaggccattg tggagccaga gaagaccaca 1260
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cactcaccag cccaggccct ctgactcc tagatccagc tgacatggaa gcacccggag 2040
gctcgtcctg gcccaatata caagtacgtt gtggaggtgc aggtggctgg ggggtgcagg 2100
gacccactgt ggatagacgt ggacaggcct gaggagacaa gcacatcat ccgtggcctc 2160
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gaagtctgt gcaaattggg gcatcacccc aacatcatca acctcctggg ggctgtaag 2760
aaccgaggtt acttgtatat cgtattgaa tatgccccct acgggaacct gctagatttt 2 820
ctgcggaaaa gccgggtcct agagactgac ccagcttttg ctcgagagca tgggacagcc 2880
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aaaaa

```

384 5

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(202)

<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111

```

aaagcccttc aaggtttact cncanctt gcaaggccca cancttggtc aaggacaaa 60
cccacaggct ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
acccatgggg canantnatg ag                                     202

```

<210> 112

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112

```

attcaagtac cttttcctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgaggt ggaagtggag 180
cccagtgaag tggaagactt cgaggctcgt gggagcgtt tctccaagtc tgctgatgag 240
agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ccttcggaaa 360
ggtgccgttc cttttgaacc ccgtgaaccc ctgncgttcg aaaggattgc ttggcttgcc 420
cgccgcggga aacggaggct ttcagaagca                                     450

```

<210> 113

<211> 1810

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1810)

<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113

```

ggggggaagg ccaagcagt accaggaaga gggagaaact tctgctcaga ccgagcgtgt 60
gccactggac ctgactctc gcctggagga gacgtggac ttcggcgagg tggaagtgga 120
gcccagtga gtggaagact tcgaggctcg tgggagccgc ttctccaagt ctgctgatga 180
gagacagcgc atgctggtcg cagcgtaagg acgaactcct ccagcaagct cgcaaacgtt 240
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cgctctctga ccccgtagcc ctgcgtcgaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgtccct tgccttctc agctgcct cc tgcgcctgt 420
gcccagctga ctggaggagg cctgtcccaa ttctgccgct ccattggaaa gcggttga 480

```

75/292

```

ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
tccttccttg taatactttc tatgtgacat ttctcttccc cttagaaaca ctgcaaattt 600
taactgtagg tatgatctct tctggg gttg actggactgc ttgggggtggg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
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tacttttttt tttttttttt tttttttact ctttgaagc tttgttttgt ggtagtctgt 1560
tttggaaga atccagtatt atctacaatt attggcaaag tttaaatgta ttttacataa 1620
cggaaagttt tttagatgtt gaaaagtaat tgaaaaagg gataggtaaa ttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaatt 1740
tctgtgcatt tttttttttt aatttgtttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc 1810

```

<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST
 R81127) gene.

<400> 114

```

gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtntccn acttttacia tgtgtacaat gtttcacat gtnccaatta atggttgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt 248

```

<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cl1/lymphoma 2
 (BCL2) gene.

<400> 115
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 caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
 gtttcanggc tgattctaaa ctggangaaa aaaaaaattt cctagtttat ttgctganga 180
 tgtcacttct tttgttactt ctttatagtt cccaccatt gattttnttt ttaatgcccc 240
 ggggtgtaca ggataacccc catattccac accgggggnac tttttttttg tcagggtttt 300
 caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggccgggg 360
 ggtcaattat ncctggacac ctcacttcaa ggcntccttt gggggtttgg gggcc 415

<210> 116
 <211> 468
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(468)
 <223> 5' terminal sequence. b-cell cll/lymphoma 2
 (BCL2) gene.

<400> 116
 aattgtgcc aaaaagcatt ttagcaattt atacaatatc atccagtacc ttaagccctg 60
 attgtgtata ttcatatatt ttggatacgc acccccacac tcccaatact ggctctgtct 120
 gagtaagaaa cagaatcctc tggaacttga ggaagtgaac atttcggtga cttccgcac 180
 aggaaggcta gagttaccca gagcatcagg ccgccacaag tgcctgcttt t aggagaccg 240
 aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtccctgggaa ctgagccggg 300
 gccctcactn gcctcctcca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
 aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
 tgggncgtgt cacttggggg cctncaggt agngcccntt ttacacgt 468

<210> 117
 <211> 6030
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(6030)
 <223> b-cell cll/lymphoma 2 (BCL2) gene.

<400> 117
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 ctttgagttc ggtgggggtca tgtgtgtgga gagcgtcaac cgggagatgt cggccctggg 540
 ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca cctggatcca 600
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 tggctccacc tggatgttct gtgcctgtaa acatagattc gctttccatg ttgttgccg 1140
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 ggatgatcaa cagggcagtg tggctocga atgtctggaa gctgatggag ctcaaatc 1860
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 tagagggaag gaacagaggc cctgggccct tcctatcaga aggacatggt gaaggctggg 2040
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 tgccttatcat ctaagatgt agctctggcc cagtgggaaa aattaggaag tgattataaa 4260
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tggtgttggg aaaagtcaca ttgccattaa actttccttg tctgtctagt taatattgtg 6000
aagaaaaata aagtacagtg tgagatactg 6030

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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

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cagcctgaat atgtgaacca gccagatgtt cggccccagc ccctc tegcc ccgagaggcc 180
ctctgcctgc tgcccacact gctggtgcca ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggctcgtaaa gagtttttgc ctttgggggt gccgtgggag aacccccagt 300
attgacaccc caggggaggg agcttgccct tcagcccccac ctt 343

```

<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 119

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```

<210> 120

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

<400> 120

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tcacatagat ttcttctctt tagtataatt gacctacttt ggtagtggga a tagtgaata 180
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atatggacat ttaaattggt 319

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<210> 121

<211> 2372

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

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ttggccagta tattatgact aaacgattat atgatgagaa gcaacaacat attgtatatt 540
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accgtgttag ccaggatggt ctgactctcc tgacctcgtg atccgcccac ctggcctcc 2340
caaagtgtg ggattacag catgagccac cg 2372
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<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 122

atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60
gacagggcga ngaggcagcc nggccgataa ncaggacgtg gccnntcggc cagggttcgc 120
tgacatgcac gctggtagct catacactgc taccctcagc acaggctgca ggaataggga 180
caagacagat gccgccggac tcttaggaag ctatttaata aatatcatcc aaanacaaaa 240
tgggaaaagg aaacaaggaa accctccggg gcacaaccac cttaggggcc aactggaatg 300
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123

<211> 258

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(258)

<223> 3' terminal sequence. src homology 3
domain-containing protein hip -55 (HIP-55) gene.

<400> 123

cgagtgaant atgttgagg aacatgttgt gtctgccgtt tttgaatacc caggggtggga 60
gcttgcccat ctgcatcccc acttcccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tcccaagggg 240
canttttaaa cagtgggtg 258

<210> 124

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 5' terminal sequence. src homology 3
domain-containing protein hip -55 (HIP-55) gene.

<400> 124

gccagggctc agtgggcaag ggetctgtgc cgtngncctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgagg tgatcgacga 120
aggctggtgg cgtggetatg ggccggatca tntgttngca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagtgt acattcagca ctcttcagg gaatagggac 300
ccccagttga ggattgaggc ntcagggttc cctccgntt gggcagattc agccttttca 360
ccccaatgg cagcaattgg ontgggtgat ttcccacaaa tcnttcttgg cattcccccg 420
acctttccca gacagtgttg ttt 443

<210> 125

<211> 1331

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain-containing protein
hip-55 (HIP-55) gene.

<400> 125

```

atggcggcga acctgagccg gaacgggcca gcgctgcaag aggcctacgt gcgggtgggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgcggtggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gaccccaact ctggactgcc caaatttgtc 240
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gtcagcacca tggccagctt cctgaagggg gcccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcctcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcagg gacgtgggac cccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttcttg 540
gccaaagcag agaaggagga ggagaaccgt cggctggagg aaaagcggcg ggccgaggag 600
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agagaaaaaa c 1331

```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```

gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag cccaatccc aacccacact ccaggccaat acatgcccct 120
gggactggct cagtcccagc accaccctgc aggtcccaac aaggtgggtt ttgtcccctc 180
tcactccttc cagctcatcc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggggtggga gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gaggncccg gaggacggcc ttgggtnttg g ggtaagggc 360
ttaanccagt cnnggctttg gtaagggccc ggnaagggat tcntgggna aattaaagg 420
aanccccagg 430

```

<210> 127

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(339)
<223> 5' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 127
gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
acatgatccc ctgtgagaag gtgtccacc c tgcccgcgat cacactgaag ctgggaggca 120
aaggctacaa gctgtcccca gaggactaca cgctcaagggt gtcgcaggcc gggaagaccc 180
tctgctgag cggcttcatg ggcatggaca tcccgccacc cagcggncac tctggatcct 240
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tgggtttcgc gaggettgc cgcttttagt ttcccaagg 339

<210> 128
<211> 1988
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1988)
<223> cathepsin d (lysosomal aspartyl protease)
(CTSD) gene.

<400> 128
ccatgcagcc ctccagcctt ctgccgctcg cctctgcct gctggctgca cccgcctccg 60
cgctcgctcag gatcccgtg cacaagttca cgtccatccg ccggaccatg tcggagggtg 120
ggggctctgt ggaggacctg attgccaaag gcccgtctc aaagtactcc caggcgggtg 18 0
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cctccaacct gtgggtcccc tccatccact gcaaaactgt ggacatcgct tgctggatcc 360
accacaagta caacagcgac aagtccagca cctacgttaa gaatggtacc tcgtttgaca 420
tccactatgg ctcgggcagc ctctccgggt acctgagcca ggacactgtg tcggtgccct 480
gccagtcagc gtcgtcagcc tctgccctgg gcggtgtcaa agtggagagg caggtctttg 540
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ccagcgggct gaccctgtgc aaggagggt gtgaggccat tgtggacaca ggcacttccc 900
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acacacaccc acacactcgc ccgcccactg tcttgggcgc cctggaagcc ggcgcccaa 1380
gcccgacttg ctgtttttgt ctgtggtttt cccctccctg gggttcagaaa tgctgcctgc 1440

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catctccagg gagtcccctc cccggcccta ccagcgcccg ctggtgagc ccctaccca 1620
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ggaggtgggg ttgggattgg gggctggtgc cagccttct ctgcagctga cctctgttgt 1920
cctccccttg ggcggctgag agccccagct gacatggaaa tacagttgtt ggcctccggc 1980
ctcccctc 1988

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<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 129

```

gtggcgccac tcattgttct cgggtgcacgc ccgcttccca cacgtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atggtccctg gacacaggtc cccacattcc tttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tctgatggc ccccgagta atgttctca 300
ggttgtaaa cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggtttnttg gaaggagntt ttcca 385

```

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 130

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tttttttttt ttttgagaaa gggaatttca tcccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt ccccgacctc gctgtggggg ctctgttttc tctccggcgc gctctcgtc 120
tgcccgacga gtgga gaaat ctgcggggcca ggcacgcaca tccgcaacga ctatcagcag 180
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aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctcgagagacc tcttcccca cctcacg gtc 360
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aaggatattg ggctttacaa cctgaggaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactgggtccc tgatcctgga tgcggtgtcc 540
aataactaca ttgtggggaa taagccccca aagga atgtg gggacctgtg tccagggacc 600

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atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
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 gagaacaatg agtgctgcca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
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tgaaccggc 4989

<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

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<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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89/292

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aaaaaaccaa a 4691

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<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

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<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

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<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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gccatttggc tttgg cttcc ttgggaaga agtctctgtg gtagtcaggg ttttccaggg 420
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<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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94/292

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tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccacccca 5340
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```

<210> 138

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 138

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catgtaggga tattaattca atatataaat gtcacatgtc tcccaaagt caccagggt 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttatttttat ctaaacctat gtatacttct ctaagattc ttagggcttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggnc cggagtgg 378

```

<210> 139

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 139

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tgcatggatc tatgtagtat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaaat cagaatgcct gtttgtggtt tcatatgcaa taatataatt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgccta 300
ggatattttg atattttacct ttatgttggga atgctattaa atgttttccn gtgtccaaag 360
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accttatgga ttctaacaag tcctagg 447

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<210> 140

<211> 4138
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4138)
<223> tek tyrosine kinase, endothelial (venous
malformations, multiple cutaneous and mucosal)
(TEK) gene.

<400> 140
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```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

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aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atctcttaaa attcacattt aatacaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaacttta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttcta ggcaggtttt acatggggac 300
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```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

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receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

```

tcgtaattgg catcaacttc atggaaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatcttttga ctcttgcag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgc tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
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tctagttagg ggaaacaaac ttccttcaag ggttaaatgc ngtggcctgg ctaagtaccc 420
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<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

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cagatgtaaa ccaactttt tttgtaactc tactgtatgt gaacactgtg acccttgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaaga 720
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tgcaattagt gtttgaaaag attcttaata gctggctgta aatactgctt ggttttttac 1320
tgggtacatt ttatcattta tttagcgtga agagccaaca tatttgtaga tttttaatat 1380
ctcatgattc tgcctccaag gatgtttaa atctagtgg gaaaacaaac ttcattcaaga 1440
gtaaatgcag tggcatgcta agtaccaaa taggagtgtg tgcagaggat gaaagattaa 1500
gattatgtc tggcatctaa catatgatc tgtagtatga atgtaatcag tgtatgttag 1560
tacaatgtc tatccacagg ctaacccac tctatgaatc aatagaagaa gctatgacct 1620
tttctgaaa tatcagttac tgaacaggca ggccactttg cctctaaatt acctctgata 1680
attctagaga ttttaccata tttctaaact ttgtttataa ctctgagaag atcataatta 1740
tgtaaagtat atgtatttga gtgcagaatt taaataaggc tctacctcaa agac ctttgc 1800
acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg tttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcattcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980

```

```

tccatttttg ccttggtgct catcttaat g gcctaattgca cccccaaca tggaatatc 2040
accaaaaaat acttaatatg ccacaaaag gcaagactgc ccttagaaat tctagcctgg 2100
tttgagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttcccc acccccgaaa atgttcaata 2220
atgtcccatg taaaacctgc tacaaatggc agcttataca tagcaatggg aaaatcatca 2280
tctggattta ggaattgctc ttgtcatacc cccaagtttc taagatttaa gattctcctt 2340
actactatcc tacgtttaaa tatctttgaa agtttgtatt aaatgtgaat tttagaagaat 2400
aatatttata tttctgtaaa tgtaaacgtg gaagatagtt at aaactgaa gcagatacct 2460
ggaaccacct aaagaacttc catttatgga ggattttttt gccccttggtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

```

aaagtcacta agaatcattt attnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tgagagaaac ggaaccagga cacatgggga gccgagagaa aacagtcacg gccagtatgt 180
tacaggagct ggaaggtnnt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcaaac gttagtcca ggaaagacaa ctactcccag ccccatatga 300
gccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttccgct ggctaattca aagtgcaatg aactggggag ggatgggggt gatgaggaag 420
gttcgntgga cggt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgtgct ntnacagggg a gcaggctgaa ggggtcccag gtggacctgg agactctcag 60
ggtcgaaaac ggcggcagac cagcatgaca gattttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgccac aggaagcctg cagtcctgga agcgcgagg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

99/292

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttcgccgagg caccgaggca 60
ctcagaggag gcgccatgtc agaaccggct ggggatgtcc gtcagaacct atgcggcagc 120
aaggcctgcc gccgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttcgccctg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaag accatgtgga cctgtcactg 420
tcttgtaccg ttgtgcctcg ctacggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tctctatgta cataccctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta aacaaaaact aggcggttga atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcatcccgtg 840
ttctcctttt cctctctccc ggagggtggg tgggcccggc tcatgccage tacttctccc 900
tcccacttgg tccgctgggt ggtaccctct ggagggtgt ggctccttcc catcgctgtc 960
acaggcgggt atgaaattca ccccttctcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaaggg gcctcaccga gtggggggcat catcaaaaac 1080
tttgagtgcc cctcacctcc tctaaggttg ggcagggtga ccctgaagtg agcacagcct 1140
agggtgagc tggggacctg gtaccctcct ggctcttgat acccccctct gtcttgtgaa 1200
ggcaggggga aggtggggtg ctggagcaga ccaccccgc tgccctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc ccctgtacct 1320
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tgtccctccc ccttgtcttt cccttcagta ccctctcatg ctccagggtg ctctgagggtg 1440
cctgtcccac cccaccccc agctcaatgg actg gaaggg gaagggacac acaagaagaa 1500
gggcacccta gttctacctc aggcagctca agcagcgacc gcccctcct ctagctgttg 1560
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gtatatgatg ggggagtaga tctttctagg agggagacac tggccctca aatcgtccag 1680
cgaccttctc catccacccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcat acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
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taacatactg gcctggactg ttttctctcg gctccccatg tgtcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtcttcc 2040
acagctcttc ccacaatgct gaatatacag cagggtgtca ataatgatt cttagtgtact 2100
ttaaaaaaaaa aaaaaaaaaa a 2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac cccccggagt acagcttctt tggttaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcatcttg 120
gtgggtatag aagggtcct gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggttcc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tcccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtcttc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggt gaatttccac agaatgatca agttgacgac aggaaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgacag aggatcccc aaggatgcaa 300
cggattcgct gctgtg tcac tcatgactgt ttgctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttaccatgaa gaccctccta ctgttgagcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagttaa gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaacaaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgctga gtcccccttt ccctggaaac cttccaccca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

<221> misc_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150

ggttgagcac agggnacttt attgatggna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttntctg 180
gggntggtgg nccagggntn ttactccttg gaggccatnt gggc 224

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151

gcgctgagta cgctgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatc tctctgcccc ctctgctgat gccccatgt 120
tcgtcatggg tgtgaaccat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcacccttg gccaaaggta tccatgacaa ctttgggtatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359

<210> 152

<211> 1283

<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttctg acagtcagcc gcattcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtcggagtca acggatttgg tcgtattggg 120
cgcttggtca ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgccc ccatgttctg catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcatg 600
accacagtc atgccatcac tgccaccag aagactgtgg atggccctc cgggaaactg 660
tggtgtgatg gccgctgggc tctccagaac atcatccctg cctctactgg cgtgccaag 720
gctgtgggca aggtatccc tgagctgaac gggaagtcca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaagtggtg gaagcaggcg tcggaggggc ccctcaaggg catcctgggc 900
tacactgagc accagtggtg ctctctgac ttcaacagcg acaccactc ctccaccttt 960
gacgctgggg ctggcattgc cctcaacgac cactttgtca agctcatttc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgtg gacctcatgg cccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagttg 1200
ccatgtagac cccttgaaga ggggaggggc ctaggagacc gcaccttgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cggtcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcgggcttga gta ccaggcg gcggggccag 180
ctcccttant ncgccccctc ttccccctcc tgttaaatac acaaataat tatattcaat 240
ntgaatcngn tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcgangg ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t                                     361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn ggggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaagggtga agacgctcaa ggccgagaac 120
gcggggnltgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagc aa cggctntnag ctgctgcttn gggtaaggg acacgccttc 240
tggaacgttc cctgccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttccactn gggttccagg gtagcaggcg gtgggnacc cacctggggg acntaggggg 360
cgnccgcaaa ccacattngg atttccggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto -oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggtt tttgcgcaca gctgccggct ggctgctacc 120
cgccccgcgc agcccccgag aacgcgcgac caggcaccca gtccggtcac cgcagcggag 180
agctcgccgc tcgctgcagc gaggccccga gcggccccgc agggaccctc cccagaccgc 240
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcggtcaacc tggccgacct ctaccggagt ctcaaagcgc ctggggctcg 420
cggaccgcgc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgcgctc ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgtgatc acgacgacgc ctacaccccc gggacagtag ttttaccccc gcgggggtgg 600
cagcgggtga ggtgcagggg gcgcaggggg cggcgtcacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgtaccg gggggccccc ggctgggccc gggggcgtct acgcccggcc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
agggcgccgg gctgccgtcg ggaccgggag ctcgctaccg acgaccacca tcagctacct 900
cccacacgcg ccgcccttcg ccggtggcca cccggcgcag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tggagacca agagcgcac aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgccca ccaagtgcg gaagcggaag ctggagcgca t cgcgccct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgccgcct 1200
cctccgggag cagggtggcc agctcaaaca gaaggtcatg acccagctca gcaacggctg 1260
tcagctgctg cttggggtca agggacacgc cttctgaacg tcccctgccc ctttacggac 1320
accccctcgc ttggacggct gggcac acgc ctcccactgg ggtccaggga gcaggcgggt 1380
ggcaccaccc ctgggaccta ggggcgcgc aaaccacact ggactccgc cccctaccc 1440

104/292

```

tgcgcccagt cttccacct cgacgtttac aagccccccc ttccactttt tttgtatgt 1500
tttttttctg ctggaacag actcgattca tattgaatat aatatatttg tgtatttaac 1560
agggagggga agagggggcg atcgcggcgg agctggcccc gccgcctggg actcaagccc 1620
gcggggacat tgggaagggg acccccggcc cctgccctcc cctctctgca ccgtactgtg 1680
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

```

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 156

```

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60
ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcacctt tagagagacc 120
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccggg 180
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
ggtcaaagaa agcaagaccc tgcaagaggc atcccagtga ccccagaag tgactggggg 300
aaggggagcg ctatcctagg anggtggggg tgggt 335

```

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 157

```

gcctggactt gtcttgggtt ccagaacctg acgacccggc gacgcgacgt ctct tttgac 60
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120
accatgcccc acttctctgg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300
cggcaccaca gagattaact tcaaggttng ggaggagttt gagggagcag antgtgggtg 360
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
gcagaagttc ctgaaggngg aggggccccca agacntcttg gaccngagaa tttccccacg 480
t 481

```

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgtccagc ctaggagtct acggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaagggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tgggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aagggagagg gccccaagac ctctgtgacc agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accaggggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgccctg cttcactgcc ccct ccgtcc caccctctcc ttctaggata gcgctcccct 660
taccacagtc acttctgggg gtcactggga tgcctcttgc agggcttgc tttctttgac 720
ctcttctctc ctcccctaca ccaacaaaga ggaatggctg caagagccca gatcaccat 780
tcgggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
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cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa
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<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

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cgcggnntga ggggaggtgg ccccgntcc gccgangaan tcgccccg cc acccgcagag 60
cncncagagg gaccattgac cttgggctcc ccaggaaaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga ccctgtgaag ccgtctcggg gcccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tggtgctggg agggggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggagntct tgcagggggg gcgccccacc gatttcgttc aacc 344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160

```

gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccac acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccagggaa ggggagccct gagccactcc 180
ctgtgggtgg cagtcaactgt ccagggaggt cccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcc aagcacgggg ggcccagggt ttnaaggggc cagttt 416

```

<210> 161

<211> 1970

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1970)

<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161

```

aggaaacggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcgagccc ctccccggt ccagcccgtt ccggggccgc gccggacc c agcccgcgt 180
ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggctagcgc cccgccacce gcagagcggg cccagaggga ccatgacctt gggctcccc 300
aggaaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctggtgac ctgcacg tgt gagagccac attgcaagg gcctacctgc 420
cggggggcct ggtgcacagt agtgctggtg cgggaggagg ggaggacccc ccaggaacat 480
cggggctgcg ggaacttgca cagggagctc tgcaaggggc gcccaccga gttcgtcaac 540
cactactgct gcgacagcca cctctgcaac cacaacgtgt ccctggtgct ggaggccacc 600
caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgatcct gggccccgtg 660
ctggccttgc tggccctggt ggccctgggt gtcttgggcc tgtggcatgt ccgacggagg 720
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
tctgagcagg gcgacacgat gttgggggac ctctggaca gtgactg cac cacaggagg 840
ggctcagggc tccccttctt ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960
gccgtcaaga tcttctctc gagggatgaa cagtcctggt tccgggagac tgagatctat 1020
aacacagtat tgctcagaca cgac aacatc ctaggcttca tcgcctcaga catgacctcc 1080
cgcaactcga gcacgcagct gtggtcatc acgcactacc acgagcacgg ctccctctac 1140
gactttctgc agagacagac gctggagccc catctggctc tgaggctagc tgtgtccgcg 1200
gcatgcggcc tggcgacact gcacgtggag atcttcggtg cacagggcaa accagccatt 126 0
gccaccgcg acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcatc 1320
gccgacctgg gcctggctgt gatgactca cagggcagcg attacctgga catcggaac 1380
aaccgagag tgggcacca gcggtacatg gcaccgagg tgctggacga cgagatccgc 1440
acggactgct ttgagtctta caagtggact gacatctg gg cctttggcct ggtgctgtgg 1500
gagattgccc gccggaccat cgtgaatggc atcgtggagg actatagacc acccttctat 1560
gatgtggtgc ccaatgaccc cagctttgag gacatgaaga aggtggtgtg tgtggatcag 1620
cagaccccc ccatccctaa ccggttggtg gcagaccgg tcctctcagg cctagctcag 1680
atgatgcggg agtgctggta cccaaacccc tctgcccgc tcaccgcgct gcggatcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

```

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
tgctcgcccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162
<211> 407
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(407)
<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162
gtgacctgac gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgcccctcac catctcacgg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180
cacagaaccg catcaagggc tgccacgac acctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnngcagan caagnct ggg gtttttncat atggaca 407

<210> 163
<211> 1130
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1130)
<223> lim domain protein (RIL) gene.

<400> 163
tgagagtccg gctcaggctc cggctgcggc tccagcccg gatgccccat tccgtgacct 60
tgccgaggcc ttccgacctg ggcttccgcc tgggtgggccc ggacttcagc gcgcccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
ggcccagtg cctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
tccaggagcg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cagggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
ccagcgctga cccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600
aggtgtacag gatgctgcgg gagccggccc agcccgtggc cgcggagccc aagcagtcag 660
gtcccttccg ctacttgcag ggcattgctag aggcgggcca gggcggggat tggccggggc 720
ctggcggccc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgacggggct gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtaagg 840
aacgggacaa gctctacat cccgagtgt tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgttg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta cccaatgcc aaggtggaac 1020
tcgtctgagc tgggaccctg ctcccacccc tgettcttaa ggtccctgct cggccgggtg 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctctgc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

anattcggaa cgagggatcc ctcctatgtc aacgtccaga acctagacaa gccccggcaa 60
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agcccttcga agatgctctt cgcgtgc etc caccctccca gtcggtgtcc 180
atgntcagc agctccgagg ggagccctgg gttccatggg aagctgagcc ggcgggaggc 240
tgaggcactg ctggcagctt caatggggat ttccnggtac gggagagcac gaccacacng 300
gggcaatatg 310

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat 120
acccctgcc tggccccctt gcccaaatg gcaggggggc caggctgggc agcagccccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
ccccatcagc ttcatecctg gggeccatcc tgcctcctct gcctggggac gatagtccca 360
ctaccctgtg ctctctcttc ccccgatga gcaacctgag gctggccaac ccggtgggg 420
ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
gggcagccat gccagagtca ggccccctac ccctcctcca ggacatgaac aagctgagt 540
gaggcgcgag gcgcaggact cgggtggaag ggggccagct tggggcgag gaggggacc 600
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca 660
tggaaccggg ggtttcctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720
tgcgctccct ggactccaac acccgactc aggtaccag ggaggccatc agtctggtgt 780
gtgaggtgtg gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
tcagctctat cctggggagg agtaacctga aatttctgtg aatgccaatc actctcaccg 900
tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gcccaaccac 960
acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtgcct 1020
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtgt cccgaagggc 1080
ttgccaggga tgtcatcagc accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140

```

tcaggaaccc acccaaactg gtcaccctc atgacaggat ggctggcttt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg 1320
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cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
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tggacctga ggggtgtggt cggactaagg atcaccgctt tgaaagtgtc agtcacctta 1860
tcagctacca catggacaat cacttgcccc tcactctctg gggcagcgaa ctgtgtctac 1920
agcaacctgt ggagcggaag ctgtgatctg ccctagcgct ctctccaga agat gccctc 1980
caatccttcc caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggct 2040
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gtattaatgt acagagtggc ccctcacct g ggcctttcct gtgccaacct gatgccctt 2220
ccccaagaag gtgagtgtt gtcatggaaa atgtcctgtg gtgacaggcc cagtggaaac 2280
gtcaccttcc tgggcaaggg ggaacaaatc acacctctgg gcttcagggt atcccagacc 2340
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aatgatattt tatgcaaaca gttcttgga cctgaattc ttcaatgaca gggatgcaa 2460
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atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tcctcctgaa gcctctgccc 2760
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actctccag gtggatt ttg tggaggtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccca cataccatct gtagagttgg aactgcattc ttttaaagtt ttatatgcat 2940
atattttagg gctgctagac ttactttcct attttcttt ccattgctta ttcttgagca 3000
caaatgata atcaattatt acatttatac atcacctttt tgacttttcc aagccc tttt 3060
acagctcttg gcattttcct cgcctaggcc tgtgaggtaa ctgggatcgc accttttata 3120
ccagagacct gaggcagatg aaatttattt ccatctagga ctagaaaaac ttgggtctct 3180
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cgcaaaacct gcagttcctg agtaccttct acaggcccg cccagcctag gcccggggtg 3300
gccacaccac agcaagccgg cccccctct tttggccttg tggataaggg agagttgacc 3360
gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttataccaaa 3420
gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt 3480
atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tcctcgcta 3540
ggcctgtgag gtaactggga tcgcacctt tataccagag acctgaggca gatgaaattt 3600
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agcc 3664

```

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

110/292

```

gagcacaggg tnccttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggtcttac tccttgaggg ccatgtgggc atgagggtcca ccaccctggt 240
gctgtagcca aattcggtgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagcnttc gaagggtggg gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccagggg tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449

```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```

tggtcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggctg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tggtgccatc aatgaccctt tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttcaaccac ccttgagaa gggtttgggg gttcattttt 420
caaggggggg gagcccaaan ggtcttcat tttttggccc ccttttt 467

```

<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

```

ggcttgtgtt tnttntctct ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtggggcg cctcccacc agcctgagac cgctctctgc ctctctctc 120
tctctcttc tccagcatct cac ccacttt ctctccttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtcacccc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagntccac aggggctagt 300
ccctgggnt acctgc 316

```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggtcgctcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agacctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgtccct gaagccagcc ttcttccatc 240
ccagggacac cacaccca gc cttcagtcct ccccttcaca gcctctggac ccctcctcac 300
tgggccattc cctcggtgtt cccaacagc ggacataggc ccaccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aaccacagtt gttgaggctt tggttgtttg 420
ggcagttgag ttgaggtttt 440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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cctcgccgca tccactctcc ggccggccgc ctgcccgccg cctcctcc gt gcgcccgcga 60
gcctcgcccg cgccgtcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcccgcac ctccggcggc gccccgggct tcccgtcgg ctccccgctg agctcgcccg 180
tggtccccgcg ggccgggttc ggtctaaagg gctcctccag ctccgtgacg tcccgcgtgt 240
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tggggaccac ccgcacgccc tcctcctacg gcgcaggcga gctgctggac ttctcactgg 360
ccgacgcggt gaaccaggag tttctgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtcg ctctcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagt gcccagctct 540
acgaggagga gctgcgggag ctgcgggcc aggtggagg gtcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccaaagtgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tggtatgcag tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcatgaag aggagatccg tgagttgcag gctcagcttc 840
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gggatatccg ggctcagtat gagac catcg cggctaagaa catttctgaa gctgaggagt 960
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ggcacctcaa ggatgagatg gcccgccatc tgcgcgagta ccaggacctg ctcaacgtga 1260
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atggggagggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
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cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgacccctcc 1620
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gtgacctgag gcctacgctt tggctctgga gatagcccca gagcagggtg ttgggatact 1860
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aggcaggtag cctgggggac tagccctgtg gagactgggg ggcttgaaat tgtccccgtg 1980
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tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggg gggagggggc 2160
cccacctccc cagccctcc ccccccctgc tgcaggggct ctggagagaa acaataaa 2218

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

gatccacgcc cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttggttactg tctcgtgtg tactgtgaga accagccaat gcttccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccaca gtgcatggat 180
gtgtacacac ccaagtcac aagacacat cacacggatg ggcgccac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggccaaggg gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncgggtggg cttaccaggt 360
tgcagggt 367

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

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tgcgcggtc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggaact ccgtgtcccg gcatccaccg cggcacctga cccttggcgc ttgctgttg 180
ccctcttccc caccctccct aatttccact cccccaccc cacttcgcct gccgcggtag 240
ggctccggcg ctcgctgtga gcgg tcgcgc cgttccctg gaagtagcaa cttccctacc 300
ccacccagc cctggtcccc gtccagccgc tgacgtgaag atgagcagct cagaggagg 360
gtcctggatt tctggttct gtgggctccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaattctac tggactcaat gagcaggtag ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

113/292

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gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctacatgct 840
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<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

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cggaagttct gttggnatga gagagacttg tctacaggca ggnaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgtgca cggtagaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggtnagtg ggatnctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggtaagggt gggctctacc 360
ccgtccnttg agctctngtg tncactncgc ttgggggata ccntcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475
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<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```
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ccagatccga atcattatcc aggagtccgc cctggactac cgccctggatc ctgagctcca 120
gctgcactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgaccgggt 300
acttcatact tgcttgtgcc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat gggaaggcac tgggagggtt aaggcggtt 420
gaggtttaca gcccgagttg caaaaaggcg ctctattgac ccggtttgag gtgttggtt 480
ttt 483
```

<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
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ccagggcgctc ccacagccag ggccagggtc ccggggccaa ctttgtgtcc ttcgtagggc 180
aggccggagg cggcgcccg gcgggtcagc agctgcccc gctgcctcag tcctgcagc 240
ttcagcagca acagcagcag cagcaacagc aacagcagc tcagccgccc cagccgcctt 300
tcccggcggg tggccctccg cggcggggag gagcgggggc tgggggggc tggag ctgg 360
cggaggaaga gtctgcagg gaggacgtga cccgctgtg ccctaagcac acctggagca 420
acaacctggc ggtgctcgag tgcctgcagg atgtgaggga gcctgaaaat gaaatttctt 480
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
aatctgtggc cagagaggtt tgcaaatcta ctat aacaga gattaaagaa tgtgtgatg 600
aaccggttgg aaaaggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
agtatcagt tcaccagtac attaccaaga tgcagcccat catttttagt gattaccgtt 720
taatctgtgg cttcatggat gactgcaaaa atgacatcaa cattctgaaa tggggcagta 780
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gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900
aagccattct ccgggtggct gagctgtcat cggatgactt tcaacttagac cggcatttat 960
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cgcgtagaag caggctctcc tacttgta a tgtgcctgga gtcagctgta cacagagggc 1260
gacaagtcag cagtgagtc cagggggaga tgctggatta ccgacgcag ttgatggaag 1320
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cagagctaga ctacaccctc atgagggtct gcaagcagat gataaagagg ttctgtccgg 2700

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taaaccatcat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggatatcc 2880
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gaacttcgg tacttcaga accaactcac ctgacctgca actcaaaggc tttttaaga 3900
aaaccacca 3909

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<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

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attaaaatct tcttctttca ctatcgtagc tttaaactctg ttgggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaaat 360
gggtttctag gcatatgtat tatggctatt 390

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<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gcccccggtg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgcc ctggttgcgc tggttcttgc ctgcggcctg 300
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 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
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117/292

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<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtcctgc aaccccgact gccacccctc tgggaattct 60
tgccctctgc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnttcat tggtctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggcccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtgg gctctgctgt aattgccatg ggaaggagac ggttcac ant ggcagttcc 360
ttctgcactn ttcaggaaaca atttctgaa gtgtgggttg cttaaagtgt cattgagaaa 420
taaccccgag ccaggccaaa ttgaaaagtt gcctgggntt tt                                     462

```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

```

agcagctcca accagggcag ccttcctgag aagatgcaac caatcctgct tctgctggcc 60
ttcctcctgc tgcccagggc agatgcaggc gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
gggtggcttc tgatacaaga cgacttcgtg ctgacagctg ctactgttg gggaagctcc 240
ataaatgtca ccttgggggc ccacaatgc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gacccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

```

118/292

```

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca agggccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggcag 480
acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540
gatcgaagt gcgaatctga cttacgccat tattacgaca gtaccattga gttgtgcgtg 600
ggggacccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660
aacaaggtgg ccaggggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
tacttgga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900
agtccagatt tacttgga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

```

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 180

```

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggtttag aacataattt 60
aaaaaaataa aacagcaaaa gtagcaaaaa atatagacc tttttaaaaa cattttcctt 120
ttttttcttt tttgttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
caggggcca caacactgcc cccaacctgg gccttcgct caccatctc tgggtaccgg 360
gntttgggt caggcaaagc aaactagtnt cgggtttatt angccactgg naccaccttt 420
ttgggggcag aggtcacctt cattcgaggg caggangcac tgacctctt t 471

```

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

```

gctttgctgc cagccacttc atcccctccc agatgttga ccaacacccc tccctgccac 60
caggactgcc tgggggagg agtgggagcc aatgaacagg catgcaagt agagcttct 120
gagctttctc ctgtcggttt ggtctgttt gccttcaccc ataagcccct cgactntgg 180
tggcaggtgc cttgtctca gggctacagc agtagggagg tcagtgttc gtgcctcgat 240
tgaaggtgac ctctgcccc gataggtggt gccagtggct ttattaat tc cgatactagt 300
ttgctttgct gaccaaagc ctgggtacca gaggatggt aggcgaagg aggttggggg 360
cagtgttggt gccnggggcc agcccaaac tgggggcttc tgtatatagc tattgaagaa 420

```

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

cctcttgcgg ccacaggcgc ggcgtcctcg gcggcgggcg gcagctagcg ggagccggga 60
cgccgggtgca gccgcagcgc gcggaggaac ccgggtgtgc cgggagctgg gcggccacgt 120
ccggacggga ccgagacccc tcgtagcgca ttgcggcgac ctgccttcc ccggcccgga 180
gcgcgccgct gcttgaagag ccgcggaacc caa ggacttt tctccgggtcc gagctcgggg 240
cgccccgcag gcgcacggta cccgtgctgc agtcgggcac gccgcggcgc cgggggcctc 300
cgcaggcgca tggagccggt ctgcaaggaa agtgaggcgc cgccgctgcg ttctggagga 360
ggggggcaca aggtctggag accccgggtg gcggacggga gccctcccc cgccccgcct 420
ccggggcacc agctccggct ccattgttcc cgccggggt ggaggcgccg agcaccgagc 480
gccgccggga gtcgagcgcc ggccgcggag ctcttgcgac ccgcgcagga ccggaacaga 540
gcccgggggc ggccggggcg agccggggac gcgggcacac gcccgctcgc acaagccacg 600
gcggactctc ccgaggcgga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660
gagctcactg tggagtatcc atggagatgt ggagccttgt caccaacctc taactgcaga 720
actgggatgt ggagctggaa gtgcctctc ttctgggctg tgctggtcac agccacactc 780
tgaccgcta ggccgtgccc gaccttgctt gaacaagccc agccctgggg agccctgtg 840
gaagtggagt ccttcttggt ccaccgggt g acctgctgc agttgcgctg tcggctgcgg 900
gacgatgtgc agagcatcaa ctggctgcgg gacgggtgac agctggcgga aagcaaccgc 960
accgcgcatc caggggagga ggtggaggtg caggactccg tgcccgcaga ctccggcctc 1020
tatgcttgcg taaccagcag cccctcgggc agtgacacca cctactctc cgtcaatgtt 1080
tcagatgctc tccctcctc ggaggatgat gatgatgatg atgactctc ttccagaggag 1140
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gaaaagatgg aaaagaaatt gcatgcagt cggctgcca agacagtga gttcaaatgc 1260
ccttccagtg ggaccccaa cccacactg cgctgggtga aaaatgg caa agaattcaaa 1320
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tctgtggtgc cctctgacaa gggcaactac acctgcattg tggagaatga gtacggcagc 1440
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gcagggttgc ccgccaacaa a acagtggcc ctgggtagca acgtggagtt catgtgtaag 1560
gtgtacagt acccgagcc gcacatccag tggctaaagc acatcgaggt gaatgggagc 1620
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accgacaaag agatggaggt gcttcaacta agaaatgtct cctttgagga cgcaggggag 1740
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ctggaagccc tggagagag gccggcagtg atgacctcgc ccctgtacct ggagatcatc 1860
atctattgca caggggcctt cctcatctcc tgcatggtgg ggtcggtcat cgtctacaag 1920
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aagagcatcc ctctgcgcag acaggtaaca gtgtctgctg actccagtgc atccatgaac 2040
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gacgcaacag agaaagactt gtcagacctg atctcagaaa tggagatgat gaagatgatc 2340
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gtcatcgtag agtatgcctc caagggaac ctgcgggagt acctgcaggc ccggaggccc 2460
ccagggtctg aatactgcta caaccacgac cacaaccagc aggagcagct ctctccaag 2520

120/292

```
gacctggtgt cctgcgcta ccaggtggcc cgaggcatgg agtatctggc ctccaagaag 2580
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ggtgacagag gacaatgtga tgaagatagc agactttggc ctgcgacggg acattcacca 2700
catcgactac tataaaaaga caaccaacgg ccgactgcct gtgaagtggg tggcacccga 2760
ggcattatatt gaccggatct acaccaccca gactgatgtg tggcttttcg ggggtgtcct 28
gtgggagatc ttactcttg gcggtcccc ataccccggt gtgcctgtgg aggaactttt 2880
caagctgctg aaggagggtc accgcatgga caagcccagt aactgcacca acgagctgta 2940
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ggtggaagac ctggaccgca tcgtggcctt gacctcc aac caggagtacc tggacctgtc 3060
catgcccctg gaccagtact cccccagctt tcccagacc cggagctcta cgtgtcctc 3120
aggggaggat tcggtcttct ctcatgagcc gctgcccgag gagccctgcc tgcctcgaca 3180
cccagcccag cttgccaatg gcggactcaa acgcccgtga ctgccacca cacgccctcc 3240
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tccctgtccc ctttctgtg ggcaggagcc ggctgcctac caggggcctt cctgtgtggc 3360
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agggcagggt gggggcagtg ttgtgccctg tcccagccca aactgggggc tctgtatata 3840
gctatgaaga aaacacaaag tgtataaatc tgagtatata ttacatgtc tttttaaag 3900
ggtcgttacc agagatttac ccacgggta agatgctcct ggtggctggg aggcacagc 3960
tgctatatat taaaaacaaa aaagaaaaaa aaggaaaatg tttttaaanaa ggtcatatat 4020
tttttgctac ttttgctgtt ttattttttt aaattatgtt ctaaac 4066
```

<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

```
cagttatata cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagggtgtaac cagctcctcg aggagatata 120
cccccaaccac caggtcatc tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgac aagtgtcttg atatgatcca gtgtat ctat agatggcgag 240
agaccacat gtagacagaa gatctgccc tccaccaagg cagtgaagg aagatagtca 300
aaaagatctg taaaatatt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaacttgt gtgnatctgt cnggtcttct ggtttccctg gagga 415
```

<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

```
agagagccga gctctggagc ctcagcgagc ggaggaggag gcgcagggcc gacggccgag 60
tactgcggtg agagccagcg ggccagcgcc agcctcaaca gccgccagaa gtacacgagg 120
aaccggcggc ggctgtgtcg tgtaggcccg tgtgcggcg gcggcgcgagg aggagcgcg 180
agcggcagcc ggctggggcg ggtggcatca tggacgagaa ggtgttcacc aa ggagctgg 240
accagtggat cgagcagctg aacgagtgc aagcagctgtc cgagtcaccag gtcaagagcc 300
tctgcgagaa ggctaaagaa atcctgacaa aagaatccaa cgtgcaagag gttcgatgtc 360
cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgttttagaa 420
ttggtggcaa atcaccagat acaaatctact tgtttatggg agattatggt gacagaggat 480
attattcagt tgaacacagt acactgcttg tagctcttaa gggtcggtac cgtgaacgca 540
tcaccattct tcgagggaat catgagagca gacagatcac acaagtttat ggtttctatg 600
atgaatgttt aagaaaatat ggaaatgcaa atgtttggaa atattttaca gatctttttg 660
actatcttcc tctcactgcc ttggtggatg ggcagatctt ctgtctacat ggtggtctct 720
cgccatctat agatacactg gatcatatca gagcacttga tcgcctacaa gaagttcccc 780
atgagggtcc aatgtgtgac ttgctgtggt cagatccaga tgaccgtggt ggttggggta 840
tatctcttcg aggagctggt tacacctttg ggcaagatat ttctgagaca tttaatcatg 900
ccaatggcct cactgttggt tctagagctc accagctagt gatggaggga tataactggt 960
gccatgaccg gaatgtagta acgattttca gtgctccaaa ctattgttat cgttgtggta 1020
accaagctgc aatcatggaa cttgacgata ctctaaaata ctctttcttg cagtttgacc 1080
cagcacctcg tagaggcgag ccacatg tta ctgcgtctac cccagactac ttcctgtaat 1140
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gagcaacagt aactccaaag tgtcagaaaa tagttaacat tcaaaaaact tgttttcaca 1260
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ctttagaatg aaccagttca ttgcatgtc aagcgacatt gttggtcaag aaaccagttt 1380
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gtaaacatta acacctcgtg aatacaattt aacttccatt tagctatagc tttactcagc 1500
atgactgtag ataaggatag cagcaaaaaa tcattggagc ttaatgaaca tttttaaaaa 1560
taattaccaa ggcctccctt ctacttgtga gttttgaaat tgttcttttt attttcaggg 1620
ataccgttta atttaattat atgattgtc tgcactcagt ttattcccta ctcaaatctc 1680
agcccatgt tgttctttgt tattgtcaga acctggtgag ttgttttgaa cagaactggt 1740
ttttccctt cctgt aagac gatgtgactg cacaagagca ctgcagtgtt tttcataata 1800
aacttgtgaa ctaagaactg agaaggtcaa attttaattg tatcaatggg caagactggt 1860
gctgtttatt aaaaaagtta aatcaattga gtaatttta gaattttag actttaggt 1920
aaaataaaaa tcaaggcac tacataacct ctctggtaac tccttgacat tctt cagatt 1980
aacttcagga tttatttgta tttcacatat tacaatttgt cacattgttg gtgtgcactt 2040
tgtgggttct tctgcatat taacttgtt gtaagaaagg aaatctgtgc tgcttcagta 2100
agacttaatt gtaaaccat ataacttgag atttaagtct ttgggtgtg ttttaataaa 2160
acagcatgtt ttcaggtaga g 2181
```

<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185
cgaagaggat gaggaagagc tncgtgtgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccc gcggtnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagcccgga gattcag ggc agacagacc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
ggggttaaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gttcctgagg 360
aagggggcac agaac 375

<210> 186
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186
gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
gaggaggggg gtgagggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcagggtg 180
gggcacttct ccc tctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
ccctgatggg tgacttcgca ggcgtagact ttgtgtttct cgtagtctgc tttgctcagc 300
gtcagggtgc tgctgaggct ntaggggtgt gtccctgtgt tccgtgtctg tgacactctc 360
ctggggggant taccnattt gggagggcgt tatccacctt ccaactgtact ttggc ctctc 420
tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcatgagg ccgggaagnt gaaggncagt nggtgcagcc acattncttt tgatccncca 540
ct 542

<210> 187
<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MCLR) gene.

<400> 187
atcacctgca gctccatgct gtccagcctc tgcttctctg gcgccatcgc gtggaccgct 60
acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcggaag 120
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgtcttcat cgcctactac 180
gaccacgtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
gccgtgctgt acgtccacat gctggcccgg gcctgccagc acgcccaggg cattcg 296

<210> 188

123/292

<211> 1270
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1270)
<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MCLR) gene.

<400> 188
ggagaggggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catggggggac 60
accaagggcc ccctggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggctcccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
ggatcccaga gaagacttct gggtccctc aactccaccc ccacagccat cccccagctg 240
gggtgtgctg ccaaccagac aggagcccg tgcttgagg tgtccatctc tgacgggctc 300
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ctgctggtga gcgggagcaa cgtgctggag acggccgtca tctcctgct ggaggccggt 480
gcactggtgg cccgggctgc ggtgctgcag cagctggaca atgtcattga cgtgatcacc 540
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gttgccgcca tctgggtggc cagtgtcgtc ttcagcacgc tcttcacgc ctactacgac 720
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cacaagaggc agcgcgccgt ccaccagggc tttggcctta aaggcgtgt caccctcacc 900
atcctgtctg gcattttctt cctctgtctg ggccccttct tctgcatct cactcctc 960
gtcctctgcc ccgagcacc cactgtcggc tgcattctca agaac ttcaa cctctttctc 1020
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gcagttcctt acctccctg tccccgtttg tcaagaggga tggactaaat gatctctgaa 1260
agtgttgaag 1270

<210> 189
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(336)
<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189
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gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120
aagaaggagc gaggtcgnc aagaagccgg ntccgcgggc gngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgtt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
tctcaacaat atgctcaactg gaga tgacgt ttttagatac gtattgattc accagctgga 60
cattctcggg gggtnngtta ggatggtag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcaact ctcttctggg acagctcctn cgctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
gtggctgcgg ggcaattgaa aaagagccgg cgaggagtcc cccgaaactt gttggaactc 60
cgggctcgcg cggaggccag gagctgag cg gcggcggctg ccggacgatg ggagcgtgag 120
caggacggtg ataacctctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180
cgagccgcca gcggcgggac ccacgcagca cttcccgggg cgacaggagc agccccgaga 240
gccagggcga gcgcccgttc caggtggccg gaccgcccgc cgcgtccgcg ccgcgtctcc 300
tgcaggcaac gggagacgcc cccgcgcagc gcgagcgcct cagcgcggcc gctcgtcttc 360
cccatcgagg gacaaacttt tcccaaacc gatccgagcc cttggacca aactcgtctgc 420
gccgagagcc gtccgcgtag agcgtccgt ctccggcgag atgtccgagc gcaaagaagg 480
cagaggcaaa gggaaggcca agaagaagga gcgaggctcc ggcaagaa gc cggagtccgc 540
ggcgggcagc cagagcccag ccttgctcc ccaattgaaa gagatgaaa gccaggaatc 600
ggctgcaggt tccaaactag tcttcggtg tgaaaccagt tctgaatact cctctctcag 660
attcaagtgg ttcaagaatg ggaatgaatt gaatcgaaaa aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggtgatc 780
tgagagat atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840
caccatcgtg gaatcaaac agatcatcac tggtagcca gcctcaactg aaggagcata 900
tgtgtcttca gagtctccca ttagaatc agtatccaca gaaggagcaa atacttcttc 960
atctacatct acatccacca ctgggacaag ccatcttgta aaatgtgcgg agaaggagaa 1020
aactttctgt gtgaatggag gggagtgcct catggtgaaa gacctttcaa accctcgag 1080
atacttgtgc aagtgcccaa atgagtttac tggtagtcgc tgccaaaact acgtaatggc 1140
cagcttctac aaggcggagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200
catgccttc cttgtggtgc gcatcatgtg tgtggtggcc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gagccttcgg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

```
tcaatacgtat tctaaaaa cg tcatctccag tgagcatatt gttgagagag aagcagagac 1440
atccttttcc accagtcact atacttcac agcccatcac tccactactg tcaccagac 1500
tcctagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
aatcgtgatg tcatccgtag aaaacagtag gcacagcagc ccaactgggg gcccaag agg 1620
acgtcttaat ggcacaggag gccctcgtga atgtaacagc ttcctcaggc atgccagaga 1680
aaccctgat tcctaccgag actctcctca tagtgaaagg tatgtgtcag ccatgaccac 1740
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gtttgaccat caccctcagc agttcagctc cttccaccac aaccctcgcc atgacagtaa 1980
cagcctccct gctagcccct tgaggatagt ggaggatgag gagtatgaaa cgacccaaga 2040
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caagcccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctcccagag 2160
cagtaactca gagagtgaag cagaagatga aagagtgggt gaagatacgc ctttccctggg 2220
catacagaac cccctggcag ccagtcttga ggcaacacct gcctt ccgcc ttggtgacag 2280
caggactaac ccagcaggcc gcttctcgac acaggaagaa atccaggcca ggctgtctag 2340
tgtaattgct aaccaagacc ctattgctgt ataaaacct aataaacaca tagattcacc 2400
tgtaaaactt tattttatat aataaagtat tccaccttaa attaaacaat ttattttatt 2460
ttagcagttc tgcaataaaa aaaaaaaaaa 2490
```

<210> 192

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. ciliary neurotrophic
factor receptor (CNTFR) gene.

<400> 192

```
cagatgctac gccgggaagg agtacattat ccaggtggca gccaggaca atnagattgg 60
gacatggagt gactggagcg taccgcccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tgcgagagacc acgaccagca ccaccagctc cctggcacc 180
ccacctacca cgaagatctg tgaccctggg gagctgggca gcggcgggg accctcggca 240
cccttcttgg tcagcgtccc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagccc gcaccccatg aggacatgca gagcacctgc agaggancag 360
gagggcggag cttgagcctt gtagaccccg gtttctattt t ncacacggg caggaggant 420
ttttgcattn tttttnagac acaatttttt gga 453
```

<210> 193

<211> 1566

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1566)

<223> ciliary neurotrophic factor receptor (CNTFR)
gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcggcgc gaggctcggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgcctcgct gccgggggcg gtcggaaggc 120
gcggcgccgaa gcccgggtgg cccgagggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccctg aagagtgggt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctccctgtcc gtgggacctg tgtgtgtgc 300
ttgcgcgcgc cgccgcagtt gtctacgccc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtta aatgggacag acctggcccc tgacctgctc aacggctctc 480
agctggtgct ccatggcctg gaactgggcc acagtggcct ctacgcctgc ttccaccgtg 540
actcctggca cctgcgccac caagtcctgc tgcattgtgg cttgccgccg cgggagc ctg 600
tgctcagctg ccgctccaac acttacccca agggcttcta ctgcagctgg catctgcccc 660
ccccacctta cattcccaac acctcaatg tgactgtgct gcatggctcc aaaattatgg 720
tctgtgagaa ggaccagcc ctcaagaacc gctgccacat tcgctacatg cactgtttct 780
ccaccatcaa gtacaaggta tccataagt tcagc aatgc cctgggccac aatgccacag 840
ctatcacctt tgacgagttc accattgtga agcctgatcc tccagaaaat gtggtagccc 900
ggccagtgc cagcaaccct cgccggtgg aggtgacgtg gcagaccccc tcgacctggc 960
ctgacctga gtcttttct ctcaagttct ttctgcgcta ccgaccctc atcctggacc 1020
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cccaggctgc ggagaccacg accagacca ccagctccct ggacacccca c ctaccacga 1260
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gcgtcccat cactctggcc ctggctgcc ctgccgccac tgccagcagt ctcttgatct 1380
gagcccgca ccccatgagg acatgcagag cacctgcaga ggagcaggag gccggagctg 1440
agcctgcaga ccccggtttc tatttt gcac acgggcagga ggacctttg cattctcttc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac acactcacac aaggacgcca accccacctta gatgcaaaga ggattcaaaa 60.
gaacatcttt gcgttttcta ccggctcccc atcatcgta tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcttgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtgtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccaccg accctggctc aggataactn c aggtacaca cacttcctga 300
cccagcacta tgatgccaaa ccacagggcc ngggatgaca gatactgtg 349

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<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

127/292

<221> misc_feature
<222> (1)..(729)
<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195
atgatgccgt gtcagagagc aaagctcctg tccttttggc ctaatttggt gatgctgttc 60
ttgggtctac cacacctcct tttgccctcc gcaggagcct gtgttggaag agatgggtgat 120
gggcctgggc gttttgttgt tggctcttgt gctg ggtctg ggtctgaccc caccgaccct 180
ggctcaggat aactccaggc acacacactt cctgacccag cactatgatg ccaaaccaca 240
gggccgggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcatggcaa caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aaacctcaca gagaaaacct aagaataagc aagtcttctt tccaggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgttgttg cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccctg gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttccc tctgcacca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggacctttt tttctgttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt 729

<210> 196
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196
ngttactcca gccttggacc ggggctgcca ctt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggctcctg cgggccactc ggccggcccc ggacggttga cggatgaagg 120
ggaactgagc tgccgacccg gggatctcga tgccgtcctc atcctgcagg gtcccccta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc ttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgctggg ccagcattgt cttnatattc ttgccttcca gcttgcggtt gttagggttg 420
cagacctaa ccgnaccgt ttccagacca tt 452

<210> 197
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

aggacgaggc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcattg 60
aagacagtcc tatggcttcc tggctctttag acccggtctt gggacgcagg gctaccgtgc 120
agctgagggg gccgggtttt ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctccgggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggg gcctccctca ggcccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360
ccggcttcga tgggtgttt 379

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

cctgggcccgg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgctgct gtcactgccca tccattggag ccagcacccc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccgcgtccct gtgtccactt 180
ctcctgaccg ctccggccgcc accccagaag gctggagcag ggacgccgtc gctccggccg 240
cctgtctcccc tccgggtcccc gtgcgagccc acgcgggccc cgggtgcccg ccgcagccct 300
gccactggac acaggataag gccacgcgca caggccccca cgtggacagc atggaccgcg 360
gcacgctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtgggccc cgagagggg c gaggtgacat 480
ataccactag ccagggtctcg aagggtctcg tggctcagc cccaatgcc atccttgaag 540
tccatgtcct cttcctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggccccgag aggtgcttct ggctcctcagt gtaaaccagca 660
gtgtcttctc gcatctccag gccctgg gaa tcccaactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttcccaaga 780
cccagatcct tgagtgggca gctgagaggg gcccacacac ctctgctgct gagctgaatg 840
accccagag catcctcctc cgactgggcc aagcccaggg gtcactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcagcgc tcgagtggcg gccgcgtact ccagcettgg 960
tccggggctg ccacttggaa ggcggtggcg gccacaagga ggcgcacatc ctgagggtcc 1020
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ccggggatct cgaatgcgct ctcactctgc aggggtcccc ctacg tgtec tggctcatcg 1140
acgccaaacca caacatgcag atctggacca ctggagaata ctcttcaag atctttccag 1200
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ccgacgacgc catgacctg gtactaaaga aagagcttgt tgcgatttg aagtgcacca 1500
tcacgggacct gaccttcttg gaccccagct gtgaggcaga ggacaggggt gacaagttt g 1560
tcttgccag tgettactcc agctgtggca tgcaggtgtc agcaagtatg atcagcaatg 1620
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ccgagttcct gctccagtta gacagctgcc acctggactt ggggcctgag ggaggcaccg 1860
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```
cacagtgagc atgccggggc cctccatcca cccgggggag cccagtgaag cctctgaggg 2280
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ggagcctagc tcttgccaca tggagcccc tctgcccgtc gggcagccag cagaggggga 3060
gtagccaagc tgcttgcct gggcctgcc ctgtgtattc accaccaata aatcagacca 3120
tgaaacctga aaaaaaaaaa aa 3142
```

<210> 199

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(402)

<223> 3' terminal sequence. epidermal growth factor (beta-uurogastrone) (EGF) gene.

<400> 199

```
tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgtttgc tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaaat tacatttttc attgattcat cacaactcat 300
tttgcaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402
```

<210> 200

<211> 4877

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4877)

<223> epidermal growth factor (beta -uurogastrone) (EGF) gene.

<400> 200

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agctggaact ttccatcagt tcttcctttc ttttctctct ctaagccttt gccttgctct 120
gtcacagtga agtcagcca g agcagggctg ttaaactctg tgaaatttgt cataagggtg 180
tcaggatatt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240
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ccttggcagg ctgcattcag aaggtctctc agttgaagaa agagcttggg ggacaacagc 300
 acaacaggag agtaaaagat gcccaggggc tgaggcctcc gctcaggcag ccgcatctgg 360
 ggtcaatcat actcaccttg cccgggcat gctccagcaa aatcaagctg ttttcttttg 420
 aaagtccaac ctcatcaaga ttatgctgct cactcttctc attctgttgc cagtagtttc 480
 aaaatttagt tttgttagtc tctcagcacc gcagcactgg agctgtcctg aaggtactct 540
 cgcaggaaat gggaattcta cttgtgtggg tcttgcacc c tctttaattt tctcccatgg 600
 aaatagatc tttaggattg acacagaagg aaccaattat gagcaattgg tgggtgatgc 660
 tgggtgtctca gtgatcatgg attttcatta taatgagaaa agaattctatt ggggtgattt 720
 agaaagacaa cttttgcaaa gagtttttct gaattgggtca aggaagaga gagtatgtaa 780
 tatagagaaa aatgtttctg gaattggcaat aaattggata aatgaagaag ttatttgggc 840
 aaatcaacag gaaggaatga ttacagtaac agatatgaaa ggaaataatt cccacattct 900
 ttttaagtgt ttaaaatctc ctgcaaatgt agcagttgat ccagtagaaa ggtttatatt 960
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 ggctctgttg gagacatcag agaaaataac agctgtgtca ttggatgtgc ttgataagcg 1080
 gctgttttgg attcagtaca acagagaagg aagcaattct cttatttgct cctgtgatta 1140
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 cctttttggg gaccgtatct tctattcaac atg gaaaatg aagacaattt ggatagccaa 1260
 caaacacact ggaaaggaca tgggttagaat taacctccat tcatcatttg taccattgg 1320
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aaaatcacca aaaacat 4877

```

<210> 201

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(153)

<223> 3' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 201

```

attagacctc acattagga aaacatcaaa atgantcacg cagcaccctt gagatcctga 60
ggttggccca gccgagccg tgctcagaag cccccagct ccggcccca gctgcccgca 120
cgcccgcct caccagcagg caggtcccca tcc 153

```

<210> 202

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 202

```

agtgaatcgc agggagaaga gctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgctg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatc ctgagacaaa cactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaacc atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaactctg 300

```

132/292

```

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgnacag gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatccntc agtctctnt tgttgacat tttgcgtggc nt 472

```

```

<210> 203
<211> 2093
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(2093)
<223> hmt1 (hmrnp methyltransferase, s.
        cerevisiae)-like 1 (HRMT1L1) gene.

```

```

<400> 203
cactgcgctt gcgcgggttg agggcggttg ctcagtctcc tggaaaggac cgtccacccc 60
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aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcagggt 180
gactgtccca gaagtgaatc gcaggagaaa gagcctgctg agtgacagtga ggcggtgtc 240
ctgcaggagg gagtacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccacgc tcagtttttt gagaggagaa aaaattctta tcctgagaca aaccactgca 360
gattggtggt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcatoct ggacgtgggc 600
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aggacgcacg catatcagcc cgtgtaccct gtgacagtga ctgtcccccac ctcctgtgtt 1860
agtgtgtccc ttactgccgt cgctcatcca ctctgtgtgg acgtaggatt gcaca gggct 1920
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atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttgggtgcc atcgcacatg ctcaataaat attttaaatg agtgaaaaaa aaa 2093

```

```

<210> 204
<211> 431
<212> DNA
<213> Artificial Sequence

```

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt tatta aggtc tggcagatgt ggtggaggtg gaagtacaaa cccaggcctg 60
ggcctaggaa agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccctt catcccaggt tcctttcttc aacctccgcc tgcctctggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccagggn ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctctg ccagtatgaa gttggggaag cgccttttct tgtccccag aacagaacaa 360
actcttggtc tctgtgggtt ngggggaaaa ggttngggg ggtttggact taggggagaa 420
gttnagcttg a 431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

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gtccccctgcc cctgcccttg gacagtcgcc cctacagncc tttccccggg cagagaacgg 60
aatttcctga gatcctcttg cacctcccag cccaccctg gccatgggta cctcggggaa 120
catagctccg tcttcagca gcccctggga catttgccac tccttcacat ctcaggagg 180
gggcccgggaa cccctcccag gcccctacc aacaccagct gtcggagccc tgcccacct 240
atccccagca gagctttaag caagaatacc atgatccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggggtggggg tcaatggggg cacagggtac ccaggggggn 360
gggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnttaag gatttnaggt 420
tntttaancg gggtg 435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

```

agaccccagt cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
caggggcactt ccagcggtc ctcactcttc tctctcaggg aaaccgtgat gaaagcaca 240
acgtggacat gtcactcgcc cagagagatg cccagggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtctt aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggccnggac 420
atttntagaa gagcatctgc ccggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggctcc ccagtgcgcc gagtgccccg cgggccccgc gagcgggagt 60
gggaccagc ctaggcaga acccaggcgc cgcgcccggg acgcccgcgg agagagccac 120
tcccgcccac gtcccatttc gccctcgcgc tccggagtc cgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcggccagg tggctaccca ccagctgcac cagggtggtg 240
tccctgggga ggtgctgcct accctcctcc gccagcatg ccccccatcg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
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tcaccgtcct agagcttagg cctgtcttc acccctctg acccgatatg tgtgccacag 1860
gacctgggtc ggtctagaac tctctcagga tgccttttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatgtt tcatttttct gaaaaaaa 1958

```

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaagcc cccagcagct gccccagggg catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tatectgggg caaaagggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgaggtt ttic gttcga agacagaatt 360
ggacagttga ggacagttat tgtcttntt taaaagnaca aggaaggttt cagnttggtt 420
tacccecaag gag                                         433
```

<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

```
ggccccctcag ccctgctgcc cagcacgagc ctgtgctcgc cctgcccac gcagacagcc 60
agaccaggg cgccccctct ggcggctctg ctccctccga aggatgcttg gggagtggag 120
cgaagctggg cgctcctctc ccctacagca gcccccttcc tccatccctc tgttctcctg 180
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```

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137/292

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<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSR14) gene.

<400> 210

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gaccggcgta tcacacacat ctccgcggac aggaagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcattgggt cgtgagcaca ctacgtgcc agccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgacag aggaggcca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccgccac aggggtaccc attcacacac cagcgttttg 300
accagatgcg agacatgttt gatggactac gtccgaacc gtacgtgca caa ctgggaa 360
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<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSR14) gene.

<400> 211

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ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgcagccccc agactcggac 120
tcggacacag actcggagga cccgagcttc cggcgagc g cgggagggtt gctccgctcg 180
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gccatctgga gggcctggta tatccagtat gtgaagcgga ggaagagccc cgtgtgtggc 480
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138/292

```

cgcatctact acaagaagcg gctccgtaag cccagcaggg aagatgacct cctggcccct 660
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<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 212
ccttttgccct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc caccataat cttttctgcc 120
gacccctagt tccctctgct cagccaagct tggtatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207

<210> 213
<211> 1304
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1304)
<223> cd74 antigen (invariant polypeptide of major
histocompatibility complex, class ii
antigen-associated) (CD74) gene.

<400> 213
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tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctggggc ggccgacctg 120
ggccccggag agcaagtga gccgaggagc cctgtacaca ggcttttcca tctgtgtgac 180
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ggacaaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
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<210> 214
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(355)
<223> 5' terminal sequence. annexin a7 (ANXA7)
gene.

<400> 214

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aggaaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccggtt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctctatggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgacctn ggccctcttc 240
atgcctccta cgtattacga tgcctngagc tttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatttt ngtgacang atcanattca ggtaa 355

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<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

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gaaccggtc tcccgcaaga tggagccggg ttgggctgtg acgtgctgc tggggtcaga 60
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ggtcaggagt catcttttcc cccttctggt cagtatcctt atcctagtgg ctttcctcca 180
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ataaaaaatt gcatat 2176

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<210> 216
 <211> 525
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(525)
 <223> 3' terminal sequence. thrombospondin 1
 (THBS1) gene.

<400> 216
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 tcatcttggt ctgtgacatg tggtgatggt gtgatcacia ggatccggct ctgcaactct 180
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<210> 217
 <211> 5722
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5722)
 <223> thrombospondin 1 (THBS1) gene.

<400> 217
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<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

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ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctoctaattt atttcttgta catctttcta catttcatac actcattaaa aacacttaac 120
acatccaatt aaa ggttctg caaagtcttc tgctgggtgg tgctcttcat cccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta ggcgagcctc 240
actttagttt ccggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggctgc aggaatatc tcaaggctcat ggaatattag ggngtctggt ncaat cttgg 360
ggcccttttt tcttttttcg ttncatttct ccattta 397

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<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

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ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggt agacattgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180
gatcaactga gatttctata catggctata atagaaggag caaatgtat aaaggagat 240

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tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220
<211> 2287
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2287)
<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220
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gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tcgtgttaaa 240
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taaacc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
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gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgtg tcttcattga gctcaagttt 180
actgtacgtg actgcaacag ctccctggg tggcgccant tcttggaag gagactttca 240
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<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
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cggcgagagg caagggaagtg gtactgctgg actttgctgc agctggaggg gagctcggct 240
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agttgcagat gattcaaacc g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of
 metalloproteinase 1 (erythroid potentiating
 activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

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gggactggaa gcccttttca naggcttgga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

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147/292

cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360
tcctcgttng cggtttttgg ggaccnttgg aagtnttc cg cagacatttt tccatgggccc 420
gggttttaag acgaacc 437

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

gccncagatc cagcgccag agagacacca gagaaccac catggccccc ttgnagccc 60
ctggttctg gcacctgtt gttgctgtg ctgatagccc ccagcaggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagtgc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacaggtccc acaaccgnag cgaggagttt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagtttng 420
tgggttcctt gggaacagtc tgaggtttag tttagcggtt ggggtt 466

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

aggggcctta gcgtgccga tcgccgagat ccagcgccca gagagacacc agagaaccca 60
ccatggcccc ctttgagccc ctggttctg gcacctgtt gttgctgtg ctgatagccc 120
ccagcaggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300
acatccggtt cgtctacacc cccgccatgg agagtgtctg cggatacttc cacaggtccc 360
acaaccgcag cgaggagttt ctcattgtg gaaaactgca ggatggactc ttgcacatca 420
ctacctgcag tttcgtggct ccctggaaca gcctgagctt agctcagcgc cggggcttca 480
ccaagacctt cactgttggc tgtgaggaat gcacagtgtt tccctgttta tccatccctt 540
gaaaactgca gagtggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600
agggttcca gtcccgctac cttgcctgcc tgccctggga gccagggtg tgcacctggc 6 60
agtcctgcg gtcccagata gcctgaatcc tgcccgaggt ggaactgaag cctgcacagt 720
gtccaccctg ttcccactcc catctttctt ccggacaatg aaataaagag ttaccaccca 780

gc

782

<210> 226
<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(353)
<223> 5' terminal sequence. ephrin -a1 (EFNA1)
gene.

<400> 226
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120
agaagagact tgcagcagat gaccagagg tgcggttct acatagcatc ggtcacagtg 180
ctgccccacg cctcttccca cttgcctgga ctgtgctgct cctccactt ctgtgctgc 240
aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
caggcactcc aaacctgtct tgggggccac ttccagagcc cccagccctt ggg 353

<210> 227
<211> 1480
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1480)
<223> ephrin-a1 (EFNA1) gene.

<400> 227
gcggagaaag ccagtgggaa cccagaccca taggagaccc gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tctcttggc cctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacaccg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcaactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtgc accggcccag 360
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaagtgac tgtcagtggc aaaatcactc acagtcctca 540
ggcccattgc aatccacagg agaagagact tgcagcagat gaccagagg tgcggttct 600
acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
ccttccactt ctgtgctgc aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840
gtcagtatta aggttttcaa ccggaaggag gccaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
aagggggccac gtggatgggc aaagcttgc aaagatgcc cctccag gag agagccagga 1080
tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttcta gccaggctact gcattctctc ccatcctggg gcagcactcc 1260

149/292

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaat aaagcaatgt gttttttcgg 1480

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<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```

ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagtacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatattcct gctagtaaac cacagttact taccagtcca taaataaaat 170

```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```

gaattcgcgg ccgcctcttg cgggccaga gtggagtggg aggtctggag ctttgggagg 60
agacggggag gacagactgg aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcacg ccgctggctc gacgattgtg gagaggcggg ggagaggcct 180
catccatccc acccggtcgt cgccggggat tggggtccca gcgacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgccgcgc 300
cggagcccgg gacaccggcc accctccgcg ccaccacccc tcgctttctc cggcttccct 360
tggcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttccct aaatttgcct 480
caagatggaa accctttgcc tcagggcacg cttttggct g gcaactggtg gatgtgtaat 540
cagtgataat cctgagagat acagcacaaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gtttctgggt taccactcat caaccacta atttggctct 660
accagcaat ggtcfaatgc acaactattg ccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcatc gtgggaatgg tggggaatgc 780
aactctgtc aggatcatt accagaacaa atgtatgagg aatggcccca acgcgctgat 840
agccagtctt gcccttggag accttatcta tgtggtcatt gatctcccta tcaatgtatt 900
taagctgtcg gctgggcgct ggccttttga tcacaatgac tttggcgat ttctttgca a 960
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tttggttaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tggtaaccct tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgctcaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

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cttcgggttc tatttctgta tgcccttgggt gtgcaactgcg atcttctaca ccctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
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gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttcactt cttgggggtt 3000
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taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg cccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

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<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggtttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc ccctcccacc ccctaaagtt ccaaccaaag tgagaggggtc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatcccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggccttct ttatccgaga gagtgaagc gtcctctggg acttctccct ctctgtcaag 180
tttgaaacg atgtgcagca cttcaagtg ctccgagatg gagccgggaa gtacttcctc 240
tgggtggtga agttcaattc ttgga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttcca ggggcctttt ttgattttt gattccccag gggggnttgg ngaggttggg 420
ttttccgccg ggggagattt tattccatgt tcntgggtn aatttaggaa cntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2
(GRB2) gene.

<400> 232

gccagtgaat tcgggggctc agccctctct cctcccttcc ccctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaag gggggacatc ctcaaggttt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 240
atgaaaccac atccgtgggt ttttggcaaa atcccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaaggtgct ccgagatgga 420
gccgggaagt acttctctct ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatattcc tgcgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattgata actcagaccc caactggtgg 660

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cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tggttggaac tttaggggggt gggaggggggc 900
gttgatttta aaaatgcaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tcactgtgc tcctctttcc cctcctttgt ctttttttcc atcctttttt ctcttctgtc 1020
catcagtga tgacgtttaa ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaacaaaa aaaaaaaaaa ccgaattca 1109
```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

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cgcgcgctct ggctgccnng ntgtacaccg cgccggaaag tggggctccg agggggcgca 60
ctcaaaaccc tgcctttcct ttacttttac tttttttttt tttcttttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctgatctcg ctccccctt cggttctttc gaccgggtcc cccctccctt 300
tttttgttct gtttgtttt gtttgtctac gagtccacat tcctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttccca 446
```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

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ggcgctgcg gccgcggccg gggcgggcgc agggccgagc ggacgggggg gcgcggggcc 120
ccggggaggc cgcggccact ccccccggg ccggcgcggc gggggagggc gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggcctgggag cgcggcgccag tggcagcggc 240
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aagcctgcgc ccgcgcccg ctcctacccc cctgccgcg acggcgcccc cagcgcgcca 420
cccccgacg gcctgctcgc ctctcccgac ctggggctgc tgaagctggc ctcccccgag 480
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ttcctctacc ccaaggtggc ggccagcgag gacgaggagt tcgccgaggg cttcgtcaag 600
gccctggagg atttacaaa gcagaaccag ctcggcgcgg gccgggc cgc tgcgcccgcc 660
gccgcgcggc ccgggggggc ctcgggcacg gccacgggct ccgcgcccc cggcgagctg 720
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153/292

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gccccggcgg cgccgcgcc cgaagcgcc gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcggggg cgccgcgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgcccgcgc cacccccagg cgcgt tgggg ccgcccgcgc tggctgcgct caaggacgag 900
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cagggtcccg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcggggg 1260
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ttcctcgatc tcgctcccc ttcggtcttt cgaccgtccc cccctcccct tttttgttc 1800
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tttctgtttt cagtaaagtc tcgttacgcc a 1891

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<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

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accaaaagtc ttcaagccac gagcggaggg cattcctgca ggcatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaccc gaaacggaag ccccgtttaa tggaggagga tgagctgccc tcctggntca 240
ttaaggatga cgctgaagta gaaagctca cctgtgaaga agaggaggag aaaatatttg 300
ggagggggtc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg ccntcgaaga cggcatttng gaggaatng aagaggaata c ggtaagaa 420
g 421

```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```
tggcaatatt ctgccgggca ctcttaaac ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccagggtg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggctcgc taggctccgg tacttatgat tacgaatcct ttccctttatt tttttgaaat 180
ccactggcct cctaattaat tcatagtatt ctggtaattc tttccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgcctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cacctatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgcagt ttggggggga tttggtgaca gntttntcag cgggagggcg 420
gcctcttctc ttcttagg 438
```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

```
aaaaattttc tgttaccaaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatattgg ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaatgt aaaaattttg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgtcctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccagggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcaccagc gcatgggccc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagccca gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cactcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcaccttca gtctgtcca gctgcatcag 840
cttcgagctc agatttttagc ttataaaatg ctggcccagc gccagc cctt ccccgaaacg 900
ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
cagccgccgc aaccacagac gcagcaacaa cagcagcccg cccttgtaa ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gccggtgcc 1140
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agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ccttttgtag cagaccgatg agtatgtagc caatctgacc 1920
```

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
aggaagaaga aggtcgagga gaatgcagag ggtggggagt ctgccctggg accggatgga 2040
gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtac tcacacagaa 2100
accggcaagg ttctgttcgg accagaagca cccaaagcaa gtcagctgga cgccctggctg 2160
gaaatgaatc ctggttatga agt gcccct agatctgaca gtgaagagag tgattctgat 2220
tatgaggaag aggatgagga agaagagtc agtaggcagg aaaccgaaga gaaaatactc 2280
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aagcaagacg tggatgatga atacagcatg cagtacagtg ccaggggctc ccagtcctac 240 0
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gcaactgggt gtttctatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtgt aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaagat tcagattgaa acaaacaaaa agctttt 5257

```

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

```
tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccagggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgaggaggcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgcgggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgcgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatfff tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca                                     507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcc aacacaattc tggcctagga aagcgggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tcctcatcag tgggtgtgact 120
ttcttccct ccttgcatgt cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttggtggt ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cagccgggcc 360
cttgcccccc acgnaaangg ncnnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncagntca agtnccnttt ggtntnccc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttcct t                                     521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnnganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcaggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcagggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctactgctcg gggacatcta cctcttatcc 180
accttccgcc tgcccccaaa gcagggtggt gtctcttttg g cctctatctc tcgccaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaaagt ccacgccgtg aacctacagc aagcgggctt ggctgatggg 360
cgcacacaca cagttctcct gcgactccga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaact gggtgaccaa catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggctttg tggaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgaat gtccattcca aggggacgag tccatccaca gtgcagtga caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
atcctgggtg agctgcggga tgatatacga gaccaggtaa aggaatgtc cctgatccga 780
aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagcccc 840
aatccctgct tccgaggtgt ggactgcatg gaagtgtacg agtaccagc ctaccgctgt 900
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gctcacgtcg acccctgttt cccgggctcc agctgcatca acaccatgcc cggcttccac 1020
tgtgaggcct gtctctgagg gtacaagggc acacaggtgt ctggtgtggg cattgactat 1080
gcccgggcca gcaaac aggt ctgcaatgac atcgatgaat gcaacgatgg caacaatggt 1140
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cgcttgggtt tcctgggcaa ccagagccag ggctgcctcc cagcccggac ctgccacagc 1260
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tcctgccagt gtaacgtggg ctgggctggg aatgggaacg tgtgtgggac tgacacagac 1380
atcgatggct acccagacca agcactgccc tgcatggaca acaacaaaca ctgcaaacag 1440
gacaactgcc ttttgacacc caactctggg caggaagatg ctgataatga tgggtgtggg 1500
gaccagtgtg atgatgatgc tgatggggat gggatcaaga atgttgagga caactgccgg 1560
ctgttcccca acaagacca gcagaactca gatacagatt catttggtga tgcctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
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tgccctgaaa tgagcaatcc taccagaca gatgcagaca gcgacctggt gggggatgtc 1860
tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgccc 1920
cagctgcca atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catccagat tatgtgcctc ctggtcccga taactgccgc 2040
```

158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggctgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgtcc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtctaac cagggcatgg aaatcgttca gaccatgaac 2280
agtgaacctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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tgcttctccc aagaaaacat aatttgggtcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaaggggtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 242

```

cacttttatt ttnccttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaaacca aaatttggtg tcctctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aacctggac aggacccgca aggncaaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctgggtt cnggttacag gtttcagggg cattttnttt tcggaggggt tnttcccgtt 480
tcgtgagggt aggctgaggg ttntgctt

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 243

```

gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatcctg gctcactgt ccaccttc a gcagatgtg 120
attagcaagc aggagtacga cgagtcgggc cctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

ctgggaaatt gcacacacct catgctagcc tcacgaaact gggataaagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

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ctctgcgggt cgcaatggaa gaagagatcg ccgctgtggt cattgacaat ggctccggca 120
tgtgcaaagc tggttttgct ggggacgacg ctccccgagc cgtgttttc t tccatcgctg 180
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acgaggccca gagcaagcgt ggcatcctga cctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac ctctacaac gagctgcgcg 360
tggccccgga ggagcaccca gtgtgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga cttcaacac ccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgctctg ggcgaccac tggcattgtc atggactctg 540
gagacggggt caccacacag gtgcccactc acgagggcta cggcctcccc cagccatcc 600
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tgtgtacgt cgccctggac ttcgagcagg agatggccac cgcgcacatc tcctcttctc 780
tggagaagag ctacgagctg cccgatggcc aggtcatcac cattggc aat gagcggttcc 840
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cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattagcg cccagcaaca cgtcattgtg taaggaaaaa taaaagtgtc g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

160/292

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245

```

ccgccgccgg gcagctgtgc ttgctctacc tgcggcgagg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgtctg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gccccgcggg agnaagcgt tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360
gccaaaggtc agggggcaag gtcgtgacat gtgttnacce tattgaaaaa aggcagcatt 420
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

```

<210> 246

<211> 473

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(473)

<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246

```

gccctctccc atccatatcg ttttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcgggtgag 120
cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180
cttccttgct ttctgacgtg gggtc agcat cggttatcaaa ctcgatccgc gtgcatggcc 240
ccggggcggt ggatgtcgca gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300
aagcgtttct gcccgcgggg cccccacgga gcaacagccg cttgtcctcg ggctgcagtt 360
gccagtgcag gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag tttgaagggt tgcgcaaggc cgt 473

```

<210> 247

<211> 5611

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5611)

<223> integrin, alpha 6 (IT GA6) gene.

<400> 247

```

gcgcgaccgt cccgggggtg gggccgggag cagcggcgag aggaggcgaa ggtggctgcg 60
gtagcagcag cgcggcagcc tcggaccag cccggagcgc agggcggccg ctgcaggctc 120
ccgctcccc cccgtgcgt ccgcccattg ccgcccggcg gcagctgtgc ttgctctacc 180
tgctggcggg gctcctgtcc cg gctcggcg cagccttcaa cttggacact cgggaggaca 240
acgtgatccg gaaatatgga gacccggga gcctcttcgg cttctcgtg gccatgcact 300

```

```

ggcaactgca gcccgaggac aagcggctgt tgctcgtggg ggccccgcgc ggagaagcgc 360
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162/292

```

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tgtttccctag ctgtgtgaat acctgctc ac gtcaaatgca tacaagtttc attctccctt 4140
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```

<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

```

cctttattca agagaccaga tgggttgccc caggatccgg ctgccagacc ctgaggccaa 60
gcacgngtgg agaccacagn acctgggcct gccnttgccc tgagctgcag cctcggcccc 120
aggatcctgn tcacagntca ccgcaggnca gngncaggaa gcagccctgg gggantggaa 180
cgntgctatt gattcattaa aaaaagaaaa gaaaan taca ccaaggttcc atntccccg 240
tgacaggtgg gcctnagggg tcggggtnac cccccccag natggcagca tgattntnt 300
acaatcaatc catcatntgg ggcacagggt gggttttcggg ggctatttnt tggctttggc 360
gaaattncgg gntggggtaa tgggtnggcc tccagggtta aggcca 406

```

<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2102)

<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

```
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ggagcgctgg ggcagcatga agtgcctggt cacgggcggc aacgtgaagg tgctcggcaa 120
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cgttgccctg agctgcagcc tcggccccag gatcctgtc acagtcaccg cagggtgcagg 2040
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at 2102
```

<210> 250

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250

tccaatatatt attattctga caggtttaga atactaggat aaataagtaa tatttntct 60

```

tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
catcagaatt ttaatagaca gtagccagcg tccttggtggc cagtgtgagt gacttctcac 180
agctgcaaac accctggggcc agatttctta aaacagctac atgacaaaaa caatgctatt 240
gacatccaat aatgctaaag cctgggtacc acccggtgcc cactgactgt ggn ttccaaa 300
catctctcca ctgactgtgg nttcaaccn caagznaagg gaaatgggat attccttggg 360
ctctt                                     365

```

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453).

<223> 5' terminal sequence. activating transcription factor 3 (ATF3) gene.

<400> 251

```

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gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
aagaaaacta ggcaatgtac tcttccgatg tttgtgtcac acaacactga tgtgactttt 180
atatgctttt tctcagatct ggtttctaag agttttggcg cggcgggggc tgtcaccacg 240
tgcagtatct caagatatct aggtggggcca gaagagcttg tcagcaagag ggaggggacag 300
aattctccca ggcgtt aaca caaaatccat ggggcagtat ggatgggcag gtccntctgt 360
tggcaaaactc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
agggtttagg ggcttttcca cttcaatgtc tta                                     453

```

<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3) gene.

<400> 252

```

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gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720
aagcagcatt tga tatacat gctcaacctt catcgcccca cgtgtattgt ccgggtcag 780

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165/292

```

aatgggagga ctccagaaga tgagagaaac ctctttatcc aacagataaa agaaggaaca 840
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gtttgcagct gtgagaagtc actcacactg gccacaagga cgctggctac tgtctattaa 1920
aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
atcttctgta agagaaaata ttacttattt atcctagtat tcctaacctg tcagaata at 2040
aaatattgtg gtaaaa                                     2056

```

<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

```

acatcatctc gtacatgacc acaccagcc cantacnntt tccacggccc ggccatagtc 60
attgtcctcc agcacctcag gcgccaggta ctccggggtc ccacagaagg ttttcatggt 120
ggccccgtca ctgatgccct ctttgcagag gccaaagtca gtgatcttga tgtggccatc 180
tttgtccagc atgaggtttt ccagcttgat gtcgcggtat accacgtccc gcgagtcaa 240
gtactcaaga gccgagacaa tctctgcacc ataaaaccgg gcccgctcct ctgtgaagac 300
acgctcccg ggacaggtgg gaagaacagc tcaccccggt tgggcatact ccattcaca 360
aggcacaggg cgggtcgtgg ggtctgggaa gggcattant ttcaggcggc agttgaggga 420
acgggggttc nggggtgttt ctgggagggg cccggttttt cggttgattn ttttgaggcg 480
atcttcatcc nttgggcaat tt                                     502

```

<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

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gaattccagc ggcggcgccg ttgccgctgc cgggaaacac aaggaaaggg aaccagcgc a 60
gcgtggcgat gggcgggggg agagccccgc cggagaggct ggcgggctgc cggtagacaga 120
ctgtgccctg tccacgggtgc ctctgcatg tcctgctgcc ctgagctgtc ccgagctagg 180
tgacagcgta ccacgctgcc accatgaatg aggtgtctgt catcaaagaa ggctggctcc 240
acaagcgtgg tgaatacatc aagacctgga ggccacgg ta cttcctgctg aagagcgacg 300
gctccttcat tgggtacaag gagaggcccg agggccctga tcagactcta ccccccttaa 360
acaacttctc cgtagcagaa tgccagctga tgaagaccga gagggcgcga cccaacacct 420
ttgtcatacg ctgcctgcag tggaccacag tcctcgagag gaccttccac gtggattctc 480
cagacgagag ggagga gtgg atgcgggcca tccagatggg cgccaacagc ctcaagcagc 540
gggccccagg cgaggacccc atggactaca agtgtggctc cccagtgac tcctccacga 600
ctgaggagat ggaagtggcg gtcaagcaagg caggggctaa agtgaccatg aatgacttcg 660
actatctcaa actccttggc aagggaacct ttggcaaagt catcctggtg cgggagaa gg 720
ccactggccg ctactacgcc atgaagatcc tgcgaaagga agtcatcatt gccaaggatg 780
aagtgcgtca cacagtcacc gagagccggg tcctccagaa caccaggcac ccgttcctca 840
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accgcgacat caagctggaa aacctcatgc tggacaaaga tggccacatc aagatcactg 1080
actttggcct ctgcaaagag ggcacagtg acggggccac catgaaaacc ttctgtggga 1140
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ggtgggggct ggggtgtggtc atgtacgaga tgatgtgcgg ccgcctgccc ttctacaacc 1260
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aggtcgacac aaggtacttc gatgatgaat ttaccgccc gtccatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggaccac ttccccagt 1620
tctctactc ggccagcatc cgcgagtgag cagtctgccc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715
```

<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

```
gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagcttcc ccatcttcta gaggaatca aagagcagga ggttggtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc tttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggcgggtt catggcaaga naggcaggac aggcaagggg 360
tttgacggct tagttagggg gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaaggtttg a 431
```

<210> 256

167/292

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
tgccgcccag gaccgcgacg agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60
acaaggaaga ggaatgtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120
caatattctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggaggt tgtggacaaa 240
gtcatggaaa cactggacaa tgatggagac ggcgaatgtg acttccagga attcatggcc 300
tttgttgcca tggttactac tgcctgccac gagttctttg aacatgagtg agattagaaa 360
gcagccaaac ctttcctgta acagagacgg tcatgcaaga aagcagacag caagggcttg 420
cagcctagta ggaagctgagc tttccagccg tgttgtagct aattagga ag cttgatttgc 480
tttgtgattg aaaaattgaa aacctcttcc caaaggctgt tttaacggcc tgcattcttc 540
tttctgctat attaggcctg tgtgtaagct gactggcccc agggactctt gttaacagta 600
acttaggagt caggtctcag tgataaagcg tgcaccgtgc agcccgccat ggccgtgtag 660
accctaaccg ggaagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720
actaccttta aaaaacaaag ccttatccag cattatttga aaacactgct gttcttttaa 780
tgcgcttcctc atccatgcag ataacagctg gttggccggt gtggccctgc aagggcgtag 840
tggtctcggc ctgcttcccg ggaatgcgct gatcaccagg tgaacgctca gcgctggcag 900
cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacccatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020
cctccagcac atgcggcttc cgagggcact accgggggct ctgagccacc gcgagggcct 1080
gcgttcaata aaaag 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp-binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagttttaaac tatgatttct 60
ctccacttga tgatgtctct cactctgttc cttaattac gaagtctctg aagactctga 120
acttgactga ggaatgttta aacagatacc tcttcataat tctgtaagt tttgctttta 180
actttgaata aatgtcatat ctaaacaaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgcctttc 300
tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtgagcaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggct tcttgacaa ccttttcacc tactgtatcc agagctgacg 480
tggtcatcc aaaaacaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgag 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatatcc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaaacagc gccggggcgt 240
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaagaa gcagaggccg ctgttcgttt cctttagggtc tttccactaa 360
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgagggt 420
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaaaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtgttt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtcaaacatc actaatagaa gtgatatcaa 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
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gataggctgg tttgatgtgc acgatgttgg ggagcttaac acccgactta cagatgatgt 960
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttcttccagt caatggcaac 1020
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agcaattaga actgtgattg catttgaggg acaaaagaaa gaacttgaaa ggtacaacaa 1260
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aatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640
aagaattgat gatcctgaaa caaacgcaca gaatagtaac ttgttttcac tattgtttct 2700

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agcccttggga attattttctt ttattacatt tttccttcag ggtttcacat ttggcaaagc 2760
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gctggcacag aaaggcatct atttttcaat ggtcagtgct caggctggaa caaagcgcca 4260
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cagtcgaagt ccagagcttc agagacttcg taattaaagg aacagagtga gagacatcat 4440
caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggaact gtaactgact 4560
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taataaaact aaactttcat gtg 4643

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<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

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caacctttat agtgttatgt caaataggct tgacataagc ttaaataaat atatacttta 60
aaaattataa aatatttttaa gttataattht aaaattctca ataaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
aacaatttca aagaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
ctcttatttc ccagagtttt tctgcccctt taaaaggaaac ctctggctgt tctgancctt 300
atcacatctc tgttttgact gttgggcttt ggttgggtgc cagtggttcg gccaggaaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttctt cacantccct cagggtnggg ggcggttng ggggnattacc ggcgggggg 480
tttttc 486

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<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
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tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctcaagtgtc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaggga tattttcttc caagcaaagg 180
tgaagagacc aagactctga aatctcagaa ttccttttct aactctccct tgctcg ctgt 240
aaaatcttgg cacagaaaca caatattttg tggctttctt tcttttgccc ttcacagtgt 300
ttcgacagct gattacacag ttcctgtcat aaggaaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacaggtg ttggatgccc 420
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<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ccaaaacgga aagtatttca agcctaaacc tttgggtgaa aagaactctt gaagtcata 120
ttgcttcaca gtttctctca gctctcactt tgggtgcttct cattaagag agtggagcct 180
ggctcttaca cacctccacg gaa gctatga cttatgatga ggccagtgtc tattgtcagc 240
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tctgggtagg aaccagaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420
ccaacaatag gcaaaaagat gaggactgag tggagatcta catcaagaga gaaaaagatg 480
tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
cctgtaccaaa tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600
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acaattcttc ctgctctatc agctgtgata ggggttacct gccaaagcagc atggagacca 780
tgcaagtgtat gtctcttggg gaatggagtg ctctattcc agcctgcaat gtggttgagt 840
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tcccatgtga cacaacctgt acatttgact tggaagaagg atttgaacta atgggagccc 960
agagccttca gtgtacctca tctgggaatt gggacaacga gaagccaacg tgtaaagctg 1020
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ctggagagtt caccttcaaa tcatcctgca acttcacctg tgaggaaggc ttcattgttg 1140
agggaccagc ccaggttgaa tgcaccactc aagggcagtg gacacagcaa atcccagttt 1200
gtgaagcttt ccagtgcaca gccttgtcca accccgagcg aggtacatg aattgtcttc 1260

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```

<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth
factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcggt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agaggggaaaa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatctt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

```

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```

ggagtccgag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tncgcacctc cgacgagcag acgcaggcct tcatcgatgc tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctgggag 180
caaganatct cttttgactt tggccccaac ggnagttttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc ccttcaagct tgtnttcgna 300
gaaacccaaa ctcgggggct ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt                                383

```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```

ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct ccggcctcgt 60
cgtgaagaca cagcgcatct ccccgctgta ggcttctccc acagaaccog tttcgggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacctatgt gctgggccgt 180
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gcctttcacc tgcctggacg gttcggccac catcccattt gatcaggtca acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagccctt gtatatcccc tccaaccggg tcaacgatgg 420
tgtttgtgac tgctgcgatg gaacagacga gta caacagc gccgtcatct gtgagaacac 480
ctgcaaagag aagggccgta aggagagaga gtccctgcag cagatggccg aggtcaccog 540
cgaaggggtc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaaag ctcatatgac tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
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gactcaccog gagctggaca cagatgggga tggggcggtg tcagaagcgg aag ctgaggc 900
cctcctcagt ggggacacac agacagacgc cacctcttct tacgaccgog tctgggccgc 960

```

```
catcagggac aagtaccggt ccgaggcact gcccaccgac cttccagcac cttctgcccc 1020
tgacttgacg gagcccaagg aggagcagcc gccagtgcc tctcgccca cagaggagga 1080
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gagcttgccc tcctggggc cccaccttg gtgactgcc ccaccacccc cagccct gtc 1980
cctgccacc ctcctagtgg ggactagtga atgacttgac ctgtgacctc aatacaataa 2040
atgtgatccc ccacc 2056
```

<210> 265

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. diphtheria toxin
receptor (heparin-binding epidermal growth
factor-like growth factor) (DTR) gene.

<400> 265

```
ggttctgtga cccatctgta gtaatttatt gtctgtctac atttctgc ag atcttccgtg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgcc aggcgatatt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctcccgt gtctctccc 240
tgccaagtct cagaagaggt tgggctt cca tgcctgtagc tttcctggtc cctcaccccc 300
atggccccag gccacagcg tggagactnc actttncct tgtgtcaaga catttctctn 360
aactctgnc attcttctg 379
```

<210> 266

<211> 2360

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding
epidermal growth factor-like growth factor) (DTR)
gene.

<400> 266

```
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ccaggtctgc acgcagaggg ggcgcgcaga cgggtgcccgc cggaatctcc tgagctccgc 180
cgccagctc tggtgccagc gccagtggc cgccgcttcg aaagtgactg gtgcctcgc 240
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gctgcagttc tctccgacac ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
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ggaggcggcc gggaccggaa agtccgtgac ttgcaagagg cagatctgga cctttt gaga 480
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tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360
```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

```
aggagtgcc cggctgcccc tcaccctgtg gcaagtacat ctctgcgcc gagtgccga 60
```

```

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gaacaacccc gtgaagggca ggacctgcaa ggagaggac tcagag ggct gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga cgcctacctc atctatgtgg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg gccaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtcc cagtnggaac aatgattatt 420
ccctttttca agagc 435

```

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
 lymphocyte function-associated antigen 1;
 macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
 gene.

<400> 268

```

cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgccgc ggact ccagc 60
acaccgaggg acatgctggg cctgcgcccc ccactgctcg ccctgggtggg gctgctctcc 120
ctcgggtgcg tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
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cctgactcca ttgctgcga caccggcca cagc tgctca tgaggggctg tgcggctgac 300
gacatcatgg accccacaag cctcgtgaa acccaggaag accacaatgg gggccagaag 360
cagctgtctc cacaaaaagt gacgcttac ctgcgaccag gccaggcagc agcgttcaac 420
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gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaacc tgatgcacc cgagggtggg 780
ctggagccca tgatcgaggt cgcgcctgc ccggaggaaa tcggctggcg caacgtcacg 840
cggctgctgg tgtttgccac tgatgacgac ttccatttcg cggcgacagg aaagctgggc 900
gccatcctga ccccaacga cggccgctgt ca cctggagg acaacttgta caagaggagc 960
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ggcccccttg ggaagaactg cagcgcgcg tgctc gggcc tgcagctgtc gaacaacccc 2040
gtgaagggca ggacctgcaa ggagaggac tcagagggt gctgggtggc ctacacgctg 2100

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176/292

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gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
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aaaataaaac ttcaat 2776

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<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

ccaggacct gaaggtgcta ccagctcctc ttacttggcc agctcccaag aggaagattc 60
aggccagagt cttcccactg cccatgttcg ccttccccc ccatgaaga gcttcgccgt 120
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actgtcccag caagctctga accatcacat tcaatcagt aagacagcct ccacggggac 240
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ggagaccaca aggggtgttg gaaggattnc gagagtaggt attgaaccag ntgagggtga 360
ncaaagagtt gggccatngg gggagggtt aattgaangg gacctaaac gttttttnac 420
aacagcttga cggactttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

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cggtgagggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgt 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactcctca gcacccctc 180
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agcatattct gagccttctc caaaaattga atggaaaaaa gatggaactt ttttaaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540
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178/292

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<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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ccctcttgcc tgaaatttcc accttcccat aggctgggga gggagtcagt tccagagcag 120
aggagggtga cagggttg ag gagggacttg tgagagctag aacttggcaa aatggcctag 180
cccacccttc aaaggggaaa agagggagga acaggggatg aaaagtntc cgcagccttc 240
ccttgaactc tcccctgctg ggggaggag gaggttaaag caagaccccc tgcccagggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

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<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

179/292

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cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
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acaaaagaga aaacaaaaaa taatcacaa agaaaccagc tgcccaaaag gaaccagagg 1980
tgaaaaacaa aaaaaaaa ccaaaaacaa accaaaaaa aaaaaaac tctacccct 2040
ctagagcc 2048

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<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

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ggtttcaatt aaataacagt aaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gattatattg ccaactaaaa cactgccatg tacatttttt ttcctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
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<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
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aaaacttgtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
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ctgagtgtg gggcactttg 2540

<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

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agtgaacccc attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180
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caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
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ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
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ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
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aaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaa 1608

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<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 277

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ttagattgca tgctattgta tgtctacagg gcatttgaca gccaaggnt aaatccaggt 60
gggacggtat ctaatgatgt cctgtccttc actgtccttg ccatcaccag ccacagagat 120
ccaggctttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

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<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

<400> 278

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gggatctttt tggtctctctg cctctaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccttg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagta 180
aagaggttgg tcaactggca gaaacccaac gtttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctcttg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa ttccagaaat 420

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ccttacacca agttgcacat attccataat aaagtgtgtgt gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgaggggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgagggtga 240
gtatgagacg caggtgggggt tgaatgaagg aaagttagta cnccttaggg ctacaggacc 300
ctgggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaactttt cggcctggag tgggtgtgtct aagggaactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagtgaag attcccccaa aaggaggggc 120
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180
tgttacaccc taaagcctga aacctgaacc ccantactct gacagaagaa ccccagggtc 240
ctgtagccct aagtgggtact aactttcctt cattcaaccc acctgcgtct tatactcanc 300
tcancacct gttggctgat tttggatgtt tgtggcccca tgtaagggaac cctttaattt 360
ggcattnccc aattgagaat taaccttttt gncccgaaac tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe
combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttcctgcagc 60
tgcccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttctcg accactatgc cactgactc cc tcaagtgt tccactctgc 180
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttggaaca 240
gcagctctga gcccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc 360
agttgcacaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaaccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatcca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtcagta cgggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc ctgacctagt gtggatggg 660
agaaacgcta cacgtttcgt gttcggagcc gctttaacc actctgtgga agtgcctcagc 720
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tcctgtttgc attggaagcc gtggttatct ctggtggctc catgggattg attatcagcc 840
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cctactgggc ccccccattg tacaccctaa agcctgaaac ctgaaccca atcctctgac 1140
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tgcgtctcat actcacctca ccccactgtg gctgatttgg aattttgtgc ccccatg taa 1260
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cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttccctc 1380
ccttctctt tccactacc ctccgattgt tctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 282
atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagtg aaaccatttt taatgcaggt ccagagccaa ctgcagtcct 180
gtccaatccc atagggtaca agggcctggg ctccctcttc tgtgtactgc ccgacttctt 240
catcttactg ggtccagca taaagcagga tgtccactgt ctccctcaca tgctgtganc 300
ttggncttag gaggtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(358)

<223> 5' terminal sequence. death associated protein 3 (DAP3) gene.

<400> 283

aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60
tagtcctcga ctacagtgca aggatgatgc tgaaaggaat aacaaggcct atctctagga 120
tccataagtt ggacctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccca ggttcccagt tgagagtccc gagagctatt ttcccgaac 240
caatgagaat gaccccggcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttnccttc 358

<210> 284

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 5' terminal sequence. ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 284

gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgcca aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctgggtg aaaaatcttt ctcatataag 360
tttnaaccac atttgattt ggggttcatt ttttgttttg ttttttttc aatcat 416

<210> 285

<211> 3052

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3052)

<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285

cgggtgtgaa ggccatgagt gattactggg ttgttgga aaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttcctaagag tttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gtttcaagtg tgctcttggt tcaagctgga ttatttcagt ggaactggca atcggccag 300

186/292

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgc aaccattcag tattcaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgc ggcaccatcc ctaaccattg 480
cggagaatat ggctgacctc atagatgggt actgccgggt ggtgaatgga acctcgagc 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagttgg 600
ccaacagcga aaagcaaggc atgcggacac acgccgtctc tgtgtcag aa acagatgatt 660
atgtcgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaagaga aagaatagaa cttggacgat gtattggaga aggccaatth ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc cagctttggc ggttgcaatt aaaacatgta 840
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cccgatataat ggaagatagt acttactaca aagcttccaa a ggaattg cctattaaat 1320
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gattttatcc cagcccacag cacatggtag aaaccaatca ttaccaggtt tctggctacc 1800
ctggttcaca tggaatcaca gccatggctg gcagcatcta tccaggtcag gcctctctt 1860
tggaaccaac agattcatgg aatcatagat ctgaggagat agcaatgtgg cagcccaatg 1920
tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca accatctga 1980
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ctgcagctcc accaaagaaa ccgctcgc ctggagctcc cgtcatctg ggaagccttg 2160
ccagcctcag cagccctgct gacagctaca acgagggtgt caagcttcag cccagga 2220
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ctagccttcc accagcagc aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
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tttgatttgg gttcattttt tgttttgggt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatagc ttctaaagg ggtggccaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 286
gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcntcc 240
atgggcagcc actccattgc tcaactccgn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

<210> 287
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(363)
<223> 5' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 287
catatctgga caaggcacc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtggtn aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccggtgtt gttacactct ggtacc gaggc 240
tcccgaagt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttg 300
ctgtatcttt gcagagatgt ttcgtcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363

<210> 288
<211> 1443
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1443)
<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288
gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggtcgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggccgtagga accggctccg gggcccgat aacgggccgc 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttgggtgcgg tgcctatggg acagtgt aca aggcccgta 300
tccccacagt ggccactttg tggccctcaa gagtgtgaga gtcccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagttcg tgagggtggt ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaagga catatctgga 540
caaggcacc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aaggagccta gatttccttc atgccaatg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtgggt gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720

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cagctaccag atggcactta caccctgtgt tggtacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggtggct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg cccagtgcag tcggtggtac ctgagatgga 1020
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tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgagc 1140
aatggagtgg ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
gcaatctttg cttttatctc tgaggctatg gaggtcctc ctccatcttt ctacagagat 1260
tactttgctg ctttaagtac attccctcc cactctcct tttgaggctt ctcttctcc 1320
ttccatttc tctacactaa ggggtatgtt ccctctgtc cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443
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<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

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ccgcgctgtg tgcgcctaan ctgagnggn ccaccgaga ccccttgagc accaacccta 60
gtccccgcg cggccctna ttcgctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcagaaa 180
gaagaagggt gtccatagaa cagccacagc agatgacaaa aaacttcagt tctccttaa 240
gangttagg gtaaacataa tctctggnat tgaagagggt aatatgttta caaaccaggg 300
aacagtgtc cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394
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<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

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atgcgacgga caggcgcacc cgctcaggct gactctcggg ggcgaggtcg agccaggggc 60
ggctgccctg gggcgaggc gacgtgtct caacctccac ctgcggcgg aaccgagga 120
gaggagctc agatgaaaga acaatcatg aaccag gaaa aactcgcaa actgcaggca 180
caagtgcga ttggtggaa agtgaatatg ttacaaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gcgaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgccaaac aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggctcca agaata 477
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<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tctgtcttgg nggtggccagc cacatgcca ggtcccctgc 120
cttctagccc agaattgacgg gactgggagc aacaccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg ctntggagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attcttagag gagccatcct gntccaaggg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgtcct ctcagagagg ggagatctca 360
ctctctgcca gtctgtctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v-fms)
oncogene homolog (CSF1R) gene.

<400> 292
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60
ggagaagaga gaagaggaag aggaagagga agagaggaag cggagggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgaggagct agtagctgag 240
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300
atgggcccag gatttctgct gtcctgtctg gtggccacag cttggcatgg tcagggaatc 360
ccagtgatag agcccagtgt ccccagctg gtcgtgaagc caggagcaac ggtgaccttg 420
cgatgtgtgg gcaatggcag cgtggaatgg gatggcccc catcacctca ctggaccttg 480
tactctgatg gtcacagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540
acctatcgct gcactgagcc tggagacccc ctgggaggca gcgccgccat ccacctctat 600
gtcaaagacc ctgcccggcc ctggaacgtg ctgacacagg aggtggctcg gttcgaggac 660
caggacgcac tactgcctg tctgtctaca gaccgggtgc tggaaagcagg cgtctcgctg 720
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190/292

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<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(356)
<223> 3' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 293
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tatgtngctt atatagagca ggaaaatccc tcctctccac aagggaagt ttcgttggtt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240
aatgggatta tctttnccct gcttggtat gcctgtnaaa taactgtacc agtggctttg 300
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<210> 294
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 294
gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgctcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaaagaa gggt tgtgtg ttaagacgc caagggcatt 240
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aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
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<210> 295
<211> 2957
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2957)
<223> friend leukemia virus integrati on 1 (FLI1)
gene.

<400> 295
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gactattaag gaggtctgt cggtggtgag cgacgaccag tccctctttg actcagcgta 240
cggagcggca gcccatctcc ccaaggccga catgactgcc tcggggagtc ctgactacgg 300
gcagccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagttag 360
ggtcaacgctc aagcggggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

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cagcgttagc aaatgcagca agctgggtggg cggaggcgag tccaacccca tgaactacaa 480
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agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatgggtgga 600
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tggcaaggaa ctgtgtaaaa tgaacaagga ggacttctc cgcgccacca ccctctacaa 720
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ttaaaatata tataattttg caggttaattg ttgacttttt taactatatt aagtgttaag 2880
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tctcaaaaaa aaaaaaa 2957

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<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

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```

cacccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tgttttttta gatacaaatc ccactaatga 300
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ctctctcttg ggctttatcc ctggggcagg ggagggggg 400

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<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

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cgtgtagat tttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagttagca 60
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tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaattgga 180
tgcactcaat aaatattttt ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtcacccgtt gagcctttgc ttttttttct gggaacactg aagggaagact 300
cacagccacc catgggtgtt tgaccctcca cttgccttgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacntct atggcttcgg nacaggtagn 420
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<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

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aaataccaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaaa 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaaataaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gccccccttt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaatgggt 360
tnaggcctcc ccaacttt 378

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<210> 299

<211> 317

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299
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caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
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ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
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cagcctcccc tatgccg 317

<210> 300
<211> 4071
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4071)
<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300
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ttgcattccc attggactca tgcacctccc ggatggtttt tgtttttttt gggggttctt 3900
tgggttttgt ttgtttgctt cttttccaga gtgtggaaag tctacagtgc agaaaggctt 3960
gaacctgccg gctgatttga aatactttca ccctgcgcag ggccgtatgc atcctgcaa 4020
gctgcgttat attctgtact gtgtacaata aagaagtttg cttttcgttt a 4071

```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

196/292

```

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagnataa ggcaaagnntt gccctctcag tntccngaag ggaaatggca gcttttcttc 240
cttccatggg cagccactcc attgctcact ccggatt acc ttcacacctta tgtaggataa 300
gggtgctgca gagctcgaaa gggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
nccgcagca gctttgcttc cccgactcct nccttttcag gnacccc 407

```

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

```

attcgncaca gaggaggagg tggaggaggc cttcccatca gcacagttcg tgagggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

```

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

```

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaata 60
ttaagtttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatttaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa ggttaggtgt tttatcccta ctatacaatt gttattatat 300
aggggaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccggccc 360
ntactttccc nggattgggg tttaggttac ctaaacggga aatttaggtc nccccntttg 420

```

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

```

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gtaggcgcgc gaaggtctgg ggcgccggag cggggccggc gtggcccgag ttccggtgag 180
cggacggcgc cgcgcgcaga tttgataatg ggctgcatta aaagtaaaga aaacaaaagt 240
ccagccatta aatacagacc tgaaaatact ccagagcctg tcagtacaag tgtgagccat 300
tatggagcag aaccactac agtgtcacca tgtccgtcat ctt cagcaaa gggaacagca 360
gttaatttca gcagtccttc catgacacca tttggaggat cctcaggggt aacgcctttt 420
ggaggtgcat cttcctcatt ttcagtgggt ccaagttcat atcctgctgg tttaacagggt 480
ggtgttacta tatttctggc cttatatgat tatgaagcta gaactacaga agacctttca 540
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gctacagagc cacagtacca gccaggagaa aatttataat tcaagtagcc tattttatat 1860
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agttttttaa agtttctt gc atttattatt ctcaaaagtt ttttctaagt taaacagtca 2340
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gtataactat aaaactaatt tttcttacac actaaatggg tatttgttca aaataatgaa 3060

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198/292

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gttatggcctt cacattcatt gcagtgggat atggttttta tgtaaaacat ttttagaact 3120
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gagtcctcgt ctgccgcccc ggctggagtg cagtggcgcg atctcggtc actgcaagct 3240
ctgcctccca gggtcacacc attctcctgc ctcagcctcc cgagtagctg ggactacagg 3300
tgcccaccac cagcctgggc tagttttttg tatttttagt agagacgcag tttcaccgtg 3360
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gagatatttt ccaacagctt ttcgtcttca gtgtcttaat gtggaagtta acccttacca 4380
aaaaaggaag ttggcaaaaa cagccttcta gcacactttt ttaaatgaat aatggtagcc 4440
taaacttaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
ttctcattga atgcacc 4517

```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 305

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ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcaggttgt cactggccac ttgcacagtg ctagtgagga 180
ggctgggcat ctcttctgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
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gggctgggag actcactcag gatctcatcg ctttgcctgg agg atgttcc agggctcact 360
gactcttggg cgcacaaggt gaaacagctt ggtttgaagg gggttnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttcctt ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga cttcctgttt tgcctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaagg anggaaacga caaactcaaa 120
gtccaggatg ttcacccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgct atgccatata caagccattt cccttctttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctaccccaa ctgggagagg actttttaac 360
ctgtntcttt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon-induced protein 75, 52kd (IFI75)
gene.

<400> 307
aattccggca tcgctttgct gggaggatgt tccaggctca ctgactcttg gcgcacaggg 60
tgaacagctt ggttgagtcg cccagcccat ctgaccctgt cctgcctctc cctgcactca 120
tccaggaagg aagaagcact tcagtacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcaactagcac tgtgcaagtg gccagtga 240
acctgatccc ccaaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaaccaa t gaccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctgggtcaa 420
ctccaaaaag gagacataag aaaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaa aggggtggatc aggttcctca aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaaa aggcgagaac tgaatgtgcc cgaaagtcga 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660
cgctagtac accacgaagg gtcacacaag ggcagcctc acctgggcat ggcacccaag 720
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aggtcatgat gaggttccaa aaggcaagaa ctaaagtgtc ccgaaagtcc agatcgaaag 840
aaaagaaaaa ggagaaagat atctgttcaa gtcaaaaag gagatttcag aaaaatattc 900
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cctgtgtgta ggcgaaaggg attttatata agaagaaaat gaaacacgga tcctcagtga 1020
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aagggaaggaa cgcaaagaac tggaaacgga atatacgttg tgaaggaaatg acctaggag 1140
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tctgtgcgg tacttgtcca cgagtcttcc atgaggactg tcacatcccc cctgtggaag 1260
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atttaattatt cgagattacg gtgagccttt caggaagcaa tgtggttga cctggttaag 1500
ggaaaggctg attacggaat tgtacacggt ggcccgaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

```
gttannncnan tnnatttttt aagagagagg caatttttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccac cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
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ctggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagacct 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

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gaactcatca tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggaccatt caagaaagtc cggaagtctc tggctcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tacccttgcc gacaactgcc cttcaaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggttct 240
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ctgcccctat gtccagtgc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacacttt 420
cgggac 426
```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

<400> 310

```
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cggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcact accaggacac 180
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```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth
factor, beta receptor iii (betaglyc an, 300kd)

(TGFB3) gene.

<400> 311

```

cccagactca aggagttggt aaagggtaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa ttgacacctt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcacct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccataacttg catacaccac tggcaaaatg tcttaatggc 360
aaattttgta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc                                     442

```

<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth factor, beta receptor iii (betaglycan, 300kd) (TGFB3) gene.

<400> 312

```

taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt ttccaatct cagcactgtc ttgngngaatt 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca ttgcatctt 240
gctagagttt gggttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta                                     315

```

<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

```

tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg cttcaaact 60
gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga ctttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttgagg aaataaaaat gacttcccat 360
tatgtgattg ccatctttgc cctgatgagc ttctgtttag cca ctgcagg tccagagcct 420
ggtgcactgt gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagc agaggcaca ctgggctgcc acaggagggtg 540

```

203/292

catgtcctga atctcgcaact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
cacctgaatc ccatctcttc a gtccacatc caccacaagt ctgttgtgtt cctgctcaac 660
tccccacacc ccctgggttg gcatctgaag acagagagac ttgccactgg ggtctccaga 720
ctgttttttg tgtctgaggg ttctgtggtc cagttttcat cagcaaatc ctccttgaca 780
gcagaaacag aagaaaggaa cttcccccat ggaaatgaac atctgttaaa ttggggccga 840
aaagagtatg gagcagttac ttatttcacc gaactcaaga tagcaagaaa catttatatt 900
aaagtggggg aagatcaagt gttccctcca aagtgaaca tagggaagaa tttctctca 960
ctcaattacc ttgctgagta cttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
cagccccaga atgagggaagt acacatcatc gagctaata ccccaactc taaccctac 1080
agtgttttcc aggtggatat aacaattgat ataagacct ctcaagagga tcttgaagt 1140
gtcaaaaaatc tcatctgat cttgaagtgc aaaaagtctg tcaactgggt gatcaaatc 1200
tttgatgtta aggaagcct gaaaattatt gctcctaaca gtattggctt tggaaaagag 1260
agtgaagat ctatg acaat gaccaaata ataagagat acattcctc aaccaagg 1320
aatctggtga agtgggctt ggacaatggc tatagtcca taactcata cacaatgg 1380
cctgtggcaa tagtatttca tcttcggctt gaaaataatg aggagatgg agatgaggaa 1440
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agcgtggata ttgccctgtc tgtcaaatg t gacaatgaga agatgategt ggtgtgaa 1740
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tgcaaggcca agatgaatgg cacacactt gttttggagt ctctctgaa tggctgcgg 1860
actcgcccc ggtggtcagc ccttgatggt gtggtctact ataactccat tgtgatacag 1920
gttccagccc ttggggacag tagtggttgg ccagatggt atgaagatct ggagtcagg 1980
gataatggat ttccgggaga tatggatgaa ggagatgct cctgttcac ccgacctgaa 2040
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aaggctgaac aagaactgg atttgccatc caaacgtgt ttatctctc atattcgaa 2280
cctgatagga tgtctcatta caccattatt gagaatatt gtcctaaaga tgaatctgt 2340
aaattctaca gtcccaa gag agtgcaactt cctatccgc aagetgacat ggataagaag 2400
cgattcagct ttgtcttcaa gcctgtctc aacacctcac tgcctttct acagtgtgag 2460
ctgacgctgt gtacgaagat ggagaagcag cccagaagt tgcctaagt tgtgctct 2520
gacgaagcct gcacctcgct ggagcctcg ataactctgg ccatgatgca gaataa gaag 2580
acgttcacca agcccttgc tgtgatccac catgaagcag aatctaaaga aaaaggcca 2640
agcatgaagg aaccaaattc aatttctcca ccaatttcc atggtctgga caccctaacc 2700
gtgatgggca ttgcgtttgc agcctttgtg atcgagcagc tctgacggg ggcttgttg 2760
tacatctatt ctacacagc ggagacagca ggaaggcagc aagtcaccac ctccccgcca 2820
gcctcggaac acagcagtc tgcccacagc atggcagca cgcagagcag gccttgctcc 2880
agcagcagc cggcgaagc caaccaggc ccaaccaggc ccagcccagc 2940
tcagctcagc tactccaagg gcaggaccaa tggctgagcc tctgttccag actcagagg 3000
ctggattttg gttcccttgt aaagacagag tgaatttcag tataaagatc acccggtgta 3060
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tcatgtgaga aagctaaaat ggtggtcttc tccaccagc cctcacaggc ttgggggtt 3180
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agagaaaatt tgaatgtct cttatgctt ta gagttgca acttaagtat atttggtagg 3900
gtgagtggtt ccaactcaaaa tatgtcaact taataatatt taggccttt cataaaacc 3960
aaactgtagc aagatgcaaa tgcattggca atctgtcgg ctccagttg ttatctgaat 4020
agtgtcacca attccaccaa gacagtgtg agattggaag ggcactcat ttgattgcc 4080
ttacttctct tgccttaaat atatcccata tatttaatat gtcaaaaagg gcttgagg 4140
aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtatacc 4200

tccttggt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacctt tccctaatac ttatnggtn acctctaggc ctgtgtgcgg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttga ggggcaggtc tggcctttcc 180
tgggtcagca tagggcacc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agtcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcggtgca ctgccagggt tccagccagc gggacaaant 360
ttccccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcgggt gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtgggtcctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttcacccac ctggcttga tcaacacccc ccggaagag 240
ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc_feature
<222> (1)..(937)
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316
cgcgccccc gggctcactt ggcgctgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagcccctga cttcaaggcc acagcgggtg ttgatggcg cttcaaagag gtgaagctgt 180
cggactacaa agggaaagtac gtggctcctt ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtcggg cgtctcgggt gactc tcagt tcacccacct ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc ccttgaaca tccccctgct tgctgacgtg accagacgct 420
tgtctgagga ttacggcgtg ctgaaaaacg atgagggcac tgcttacagg ggcctcttta 480
tcatcgatgg caagggtgtc cttcgccaga tcaactgtta tgatttgcct gtgggacgct 540
ccgtggatga ggctctgcgg ctgggtccagg ccttcagta cacagacgag catggggaag 600
tttgtccggc tgcttggaa cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatatct ctccaaacac aattaggctg gctaacggat agtgagcttg tgccccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgacctcagg 780
aaaggccaga cctgccctc caaaatccac agtatggag cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgccctc ccccaagccc acccagccgc 900
acacaggcct agaggtaacc aataaagtat tagggcc 937

<210> 317
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317
gttagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gcccgctccg tgccagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcact ccggtggtca cctgtactcc cagctgcact gctta cacgt 240
cttccttctg cttcacctac cccgaggctg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttcctc tgactcgttc agctnaccga cgggtgctggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451

<210> 318
<211> 2084
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2084)
<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.

<400> 318

```

aaccgcatct gcagcgagca actgagaagc caagactgag ccggcgggccg cggcgcgagcg 60
aacgagcagt gaccgtgctc ctaccagct ctgcttcaca gcgcccacct gtctccgccc 120
ctcggccctt cgcccggtt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgagc gtcac ctcc cgctgcagca gcgctcccc ggccggggat agcctctctt 240
actaccactc acccgagac tccttctcca gcatgggctc gcctgtcaac gcgcaggact 300
tctgcacgga cctggcgtc tccagtgcc aattcattcc caccgtcact gccatctcga 360
ccagtcggga cctgcagtgg ctggtgcagc ccgcccctgt ctctctgtg gccccatc gc 420
agaccagagc ccctcaccct ttcggagtcc ccgccccctc cgtcggggct tactccaggg 480
ctggcgttgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaaggga aggaataaga 600
tggtgcagc caaatgccg aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctaccgacc tgcctgcaag atccctgatg 780
acctggcctt cccagaagag atgtctgtgg ctcccttga tctgactggg ggctgccag 840
aggttgccac cccg gagtct gaggaggcct tcacctgcc tctcctcaat gacctgagc 900
ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
ttgatgactt cctgttcca gcatcatcca ggccagtggt cctgagaca gcccgctccg 1020
tgccagacat ggacctatct gggctcttct atgcagcaga ctgggagcct ctgca cagtg 1080
gctccctggg gatggggccc atggccacag agctggagcc cctgtgact ccggtggtca 1140
cctgtactcc cagctgact gttacacgt ctcccttctg ctccacctac cccgaggctg 1200
actccttccc cagctgtgca gctgccacc gcaagggcag cagcagcaat ggccttcc 1260
ctgactcgtc cagctcacc acgtcgtctg cctgtgagg gggcaggga ggggaggcag 1320
ccggcaccca caagtgcac tgccgagct ggtgcattac agagaggaga aacacatctt 1380
ccctagaggg ttcctgtaga cctaggagg accctatctg tgcgtgaaac acaccaggct 1440
gtgggcctca aggacttgaa agcatccatg tgtggactca agtccttacc tcttccggag 1500
atgtagcaaa acgcatggag tgtgtattgt tcccagtac acttcagaga gctggtagtt 1560
agtagcatgt tgagccaggc ctgggtctgt gtctctttc tcttctcct tagtcttctc 1620
atagcattaa ctaatctatt gggttcatta ttggaattaa cctggtgctg gatattttca 1680
aattgtatct agtgcagctg attttaacaa taactactgt gtt cctggca atagtgtgtt 1740
ctgattagaa atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata 1800
gaaataaata gctaatcca tgtactgtag ttttcttca acatcaatgt tcattgtaat 1860
gttactgatc atgcattgtt gaggtgtct gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt ttttctacct tgaggtcttt tgacatgtgg aaagtgaatt tgaatgaaaa 2040
atthaagcat tgtttgctta ttgtccaag acattgtcaa taaa 2084

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<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

```

ctgcaaagcc aatcaagaag tgttggaagg aaaaagtgtg aaagttattc ttgcatattt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangcaa cattcttctc 180
ttccctaata gctacaant gatacgtac gcaacagctc acttgaaagt gctagantca 240

```

<210> 320

207/292

<211> 457
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(457)
 <223> 5' terminal sequence. retinoblastoma -binding
 protein 7 (RBBP7) gene.

<400> 320
 agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
 agaatacacc gtttctatat gacctgggta tgacctatgc tcttcagtgg cccagtctta 120
 ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
 tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggttgc cgagtacata 240
 ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
 gtggcctttgg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
 gaagttaaac cgtgctcgtt aacatggccg cagantcctt cacatccatt gcttacaan 420
 acaccctctt gcttgatggt gttgntttt tgactat 457

<210> 321
 <211> 1946
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1946)
 <223> retinoblastoma -binding protein 7 (RBBP7)
 gene.

<400> 321
 gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
 ggagagagag agaagagcgc ctcagacctc ggtaccgcgc agcggggagg aggcaggaaa 120
 gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc ttctgacagt 180
 ggggagtggt acgcgcttgg gaaaggcagg agcgcagcgc gtcgggctgc tcttggttaa 240
 cgagaggagt ccgaggcggc ggcgaggggc gaacgaccgc acgcaagatg gcgagtaaag 300
 agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataataa atctggaaga 360
 agaatacacc gtttctatat gacctgggta tgacctatgc tcttcagtgg cccagtctta 420
 ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
 tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggttgc cgagtacata 540
 ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
 gtggcctttgg ttctgtaaca ggaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660
 aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
 cttctgatgt gttgggtttt gactatacaa aacaccctgc taaaccagac ccaagtggag 780
 aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggctatggt ctctcctgga 840
 attcaaattt gagtggacat ctcttaagtg catctgatga ccatactgtt tgtctgtggg 900
 atataaacgc aggaccaaaa gaaggcaaaa ttgtggatgc taaagccatc ttactggcc 960
 actcagctgt ttagaggat gtggcctggc acctgtgca cgagtcattg tttggatctg 1020
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 gtcacttggt ggatgcgcac actgccgaag tcaactgcct c tcattcaat cctacagcg 1140
 aatttattct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
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 ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgctg aatgtgtggg 1320

208/292

atttaagtaa aattgg ggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aacccaatg 1440
agccttgggt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaacca aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagt agctgttgcg tactgtatca tattgtagct 1740
attaggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtcctca ttttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

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cctactctga atctctgctc agaggaggca gtgactcgct ccccaccct ctcccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatccctc gggagggtctg 180
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caccctcac acaccatct ctgccatctg ctacatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

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ccatctcccc catctccctg cctgtctgcc tgcgcatcc cagcaaagat cctctggaag 120
agaccccaaga ggctccagtg cccaccaaca tgagcacagc gncagacctc ctgctgcagg 180
gtgctgctg caggtngctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc cggggccagc tctgcagctc tgagctgta g cccccggccg acaccagctg 300
ttgtccactt caaggtgtca gccagggca ttnacactga cgggacaacc aaaggaagct 360
ctttnttttc gccgccatta tccagtggaa cagcatcacc 400

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<210> 324
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 5' terminal sequence. atp-binding cassette,
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
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gagggaantg atggatttta aatggtgatt atggttacct ttttaattaa cntgtgttg 420
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ttcacagtt 489

<210> 325
<211> 5838
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5838)
<223> atp-binding cassette, sub-family c
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325
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210/292

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<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

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gcttgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttctt tgattgtcaa 300
aggttgaaat tcacatttna ntannagggg ntcnnaatca ngntcctcac taccctctac 360
ccctcancta accccctttg gggcc 385

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<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

```

ggcacgagca aganaggagt tctctgatgc agaaattatt gggctctttt agggtaagaa 60
gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
ggcttccctc tttcatctcc tgagtatgta acttgcaatg ggcagctatc c agtgacttg 180

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ttctgagtaa gtgtgttcat taatgtttat ttagctctga agcaagagt atatactcca 240
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ggcttggaga tggcaggaga gcttgtcatt gagcctgggc aatttnagca aactgatgtc 360
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ggg 423

<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
(CDH1) gene.

<400> 328

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ttgagtgtat acatgtgtgg gtgctgataa ttgtgtatt tctttggggg tggaaaagga 4740
aaacaattca agctgagaaa agtattctca aagatgcatt tttataaatt ttattaaaca 4800
attttgttaa accataaaaa aaaaaaaa 4828

```

<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tccccagtc cccacccc cc 60
gaccccgga tcatgcatcg gactacacgg atcaaaatca cagagctgaa cccccacctc 120

```

214/292

```

atgtgtgccc tctgcggggg gtacttcacg gacgccacca ctatcgtgga gtgcctgcat 180
tccttctgca aaacctgcat cgtgcgctac ctggagacca acaatactg ccccatgtgt 240
gacgtgcagg tccataaaac cggccgctg ctgagca ttc aggtctgaca aaacatttca 300
agacattgtc ttacaaattg gtccctgggg ctttttaaag atggagattg aaacggggcg 360
cgggatttct tatggcaggc gttaccctt ggacgggagg ttccccaac ggnttccaat 420
tgagggaccg ngggcgaggg ttttnggga ggcagggaga aggggggttt t 471

```

<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

```

gagagcccgga acaggaagag ggtacagctt tgtg caggtc acatgccac tgcagccctc 60
cagcctctgg tccccagagc ggacttttga agctgaactg cttttgttgc tgaagactt 120
atgttataat ttacctggg tggaccaggg tcgtacaaa gggcaacgct cccagtcctc 180
ccactcccg accccggaat catgcatcgg actacacgga tcaaaatcac agagctgaac 240
ccccacctca tgtgtgccct ctgcgggggg tacttcacg acgccaccac tatcgtggag 300
tgccctgcat ctttctgcaa aacctgcac gtgcgctacc tggagaccaa caaatactgc 360
cccatgtgtg acgtgcaggc ccaaaaacc cggccgctgc tgagcatcag gtctgacaaa 420
acacttcaag acattgtcta caaattggtc cctgggcttt ttaaagatga gatga aacgg 480
cggcgggatt tctatgcagc gtacccctg acggaggctc ccaacggctc caatgaggac 540
cgcgcgagg tcttggagca ggagaagggg gctctgagtg atgatgagat tgcagcctc 600
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ggggatgggg acaaagagaa aacagggggt cgc ttcctgc gatgccagc agccatgacc 720
gtcatgcac ttgccaagtt tctccgcaac aagatggatg tgcccagcaa gtacaagggt 780
gaggttctgt acgaggacga gccactgaag gaatactaca cctcatgga catcgctac 840
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aagcggctca ccctagccac ggtgccacc cctccgagg gcaccaacac cagcggggcg 960
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gccaccacc ctacctccc cactccccc tcgacagcca gtggggccac c acagctgcc 1140
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caccccacc aaccttacc tcaccgggga accctcacta gcaggactgg tgggtggagt 2100
tcacctggg cctagagtgg aagtgggggt gggtaacct cacacaagca cagatcccag 2160
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acactgc 2227

```

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(254)
<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180
tccttccagg gacccagcag ttgtgggtaa agcaggcaag tgggcccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(362)
<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
gccatggncg tgggtctaca cgatggaccc aaggacccca t tggactact gtgccctgcg 60
acgctgcgct gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagagggtgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
tgcgggnggt ctctagtga ggagcagtng atactgactn cccggaagtg cttctcctcc 300
tnccatatnc ctctcacggg ctatgaggta tggttngggc ancctttttc cagaaccac 360
ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2219)
<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

<400> 333

```

agccagaagg atgggggtggc tcccactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct 120
gctacatgcg gtggtgcccc ggcccttgca ggaggatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggactgccg ggcccttcac tacaacgtga gcagccatgg 240
ttgccaaact ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg 360
gtaccggggc accatggcca cgacctgggg tggcctgccc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg 480
ccgtaaccct gatggcgac c cgggaggtcc ttggtgctac acaacagacc ctgctgtgcg 540
cttcagagc tgccgcatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcggtag accgcacgga gtcagggcgc gagtgcacgc gctgggatct 660
tcagcaccgc caccagcacc ccttcgagcc gggcaagtgc ctcgaccaag gtctggacga 720
caactattgc cggaaatctg acggctccga gcgcccatgg tgctacacta cggatccgca 780
gatcgagcga gagttctgtg acctccccg ctgcgggtcc gaggcacagc cccgccaaag 840
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caccactgcg ggcgtacctt gccagcgttg ggacgcgca a atcccgcatc agcaccgatt 960
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gacgcgcgac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
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gaccccatc gactactgtg ccctgcgacg ctgcgctgat gaccagccgc cat caatcct 1380
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tccagggacc aagtgtgaga ttgcaggctg gggtagagacc aaaggtacgg gtaatgacac 1860
agtctctaat gtggcctttc tgaatgttat ctccaaccag gagtgttaaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccccctg tgggggacctg 1980
tgagggtgac tacgggggccc cacttgacct ctttaccac a actgctggg tcctggaagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgtg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggt catgagactg gggttagccc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219

```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```

gaaaggaagg caaactctgc ccccc gctca gagtcccccc aacctcact gtttcccgtt 60
gccattgatg gggaggttca cgtactcagg ggaggccagg naggcntgna gcttgggccc 120
ggcactgagg cgcgccacat atgctgagag cagggggaac gcatccaggc agccagggct 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc agggctctca aaggcttcag 300

```

217/292

ttgcccgggc agtgccttca catagtcata cttgcccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggtg 420
nctcctttt t 431

<210> 335

<211> 305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(305)

<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335

nattcgccac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccatacctgcg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336

<211> 737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(737)

<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336

ggagtttcgc cgccgcagtc ttgccacca tgccgcccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120
aggagtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgccatacag 180
ggcagctccc caagtccag gacggagacc tcaccctgta ccagtccaat accatacctgc 240
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agacctgct gtcccagaac caggagggca agaccttcat tgtgggagac cagatctcct 480
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tggatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgcccg cccaagctca 600
aggccttcc ggcctcccct gagtacgtga acctcccat caatggcaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gagtttgcc tcccttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggncgtgt gttgaaacag gccacgtaaa gcaactctct aaagggtcaaa ccaccataga 60
tttgaatctg ctggtcattc gccatctgga tttttaactg aatgaatctc atgggttttaa 120
ccaaacatgc atgtaatcct gaataccatg anttaaagtc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tcnnggggtt ttcttagggt aggcgtgagga ctcaggggct tatctcacct tctcaggaat 360
gctttttgaa gg 372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tcacgtacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca ttccggtgac ttccgcatca ggaaggctag agttaccag agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtccctggaa ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtgtggt ctccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcctttttt aagtggga 508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```

tttttttant caaaagtttg aaattcaagt aactttatnt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctagggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttacaggtata tgctgggcac cttaggaagn 300
cagttctcaa agggnccttag gttttatntn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt ggggngggcc aggtaggntt tttagggtgc cccntatccc 420
ganttttata ctctncaccg gggggg 445

```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```

gctccagcgt tgtaaacctg cagagatgga ctgctccac gtctcttttg tgcagctcac 60
ctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tgggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat taccataagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagtt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437

```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```

aggtctcagc cggctcgtgc gacgttggcc cgctcgctct gaggtccttg aagccgaaac 60
tagctagact ttcctccttc ccgcctgcct gttagcgcggt tgttgccact ccgccaccat 120
gttcgaggcg cgcttggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcgggt gtaaacctgc agagcatgga 240
ctcgtccac gtctcttttg tgcagctcac cctgcgggtc gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

```

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc ctgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatgtgta cctctaagta catatgtaga 1020
tattgttttc tgtaataaac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c 1231

```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 342

```

ttttttttt aaacacacan gttttcacgc ttagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aagggttaagt gttctcggtt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggagggggaa gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtacttttt tac 383

```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcatct ttgtcctaac atgagtgtct gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt cccttccctt cccacatatc atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gtttgtaggt aatgggggtc ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaattttt ctgtttattt aagg atgccg tggatttggt 420
aaaaggctctg gtattttgcg gggatgtctg gggtaggga ggccttacc ataggggntg 480
ggg 483

```

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaaatc tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
gatttttaca tcattacaca gatatgcat tttcattagt tgcattcattg ttataaactg 240
gtatatgtct cgagtccacg gtatgcaccc taaagagacc acccgctcagc tgagcttagc 300
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaatca 420
tgactggtat tgttttgaat gccatttgcc tggagagggtg ttgatattgtg acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
ctggcagtgcc ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600
cacatacctc agattcattg tctcccgcac gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggctggtg cactcagctg tggacgttcc 720
caccattcaa gagaaagtga atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780
tgcccaattg cttctccaca ataccgtgat tttctatgga gcagacagtg agcaagctga 840
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttacc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaaagaa gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtcgc acgtgaagcg 1140
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
aggagatatt tggaaatcta agaagtagga ccgaggtgag gaagaggcag aatccagtat 1260
ctcctccacc agtaatgagc agctaaaggc cactcaagaa ccaagagcaa agaaaggacg 1320
acgtaatcaa agtgtggagc caaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaatacca cgatgcctca gccc atcgaa aaagtctccg tgcactca 1440
gacaaagaag ttaagtgcct cttcaccaag aatgctgcac cggagcacc agaccacaaa 1500
cgacggcgtg tgtcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560
agaccggatg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctgcgt tctgaaatgg aagaagaaaa gagacaagct gtaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaaag gaaaagtgtg aggaggaatt 1740
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgattttctc agaccaagaa 1800
gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
ctactgctcc atcaagtgc agcaggagca ctggcacgag gagcacaagc gcacctgccg 1920
ccggaagaaga tgaagctggc ccttcccga gtcacccga tgattactct tttcagacac 1980
agcgggtttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
ccttttaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcagggg taaaagtaac atcagtgag ggtattattt taaataaatt 2160
ttaattgaga atttgttgca ttttcagcaa attttaaaac atttttaggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa aacagtgaa tacaagtga ttttaacaaag 2 280
aaaccttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
ctgttcaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460
gggttgacac agcagggcta gtccctgata tttttt ctta aatatttccc aattgtgttt 2520
ttcattattt cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580
ttaaaattgc agggaaactg ggtaatcttt tactgagctg gatcttagag aaaaatgaata 2640
tttaaatatt aaagtttgcc acatttcac tttgtcctaa catgagtgtc tgaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix

metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcattgcagca tcttgagtgg tagcgtcgat ctacagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaacgcc agtagtcct 120
gcctcggaag aagtagatct tgttcttctc gggacccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggaactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttggga agaaccacaaat gtgggcccgg cttaccacgc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca
```

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gccccggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgetgctgct gctccagccg ccgcccgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtagcccg cactgcccc tgccacgcag gaagcccccc ggccctgccag 240
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccga 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gatecttcgg tccccatggc agttggtgca ggagcagggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cactttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttcg ccaggtactg gcatggggac gacctgccgt ttgatgggccc 540
tgggggcatc ctggcccacg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcagggtggc 660
agcccagtaa tttggccacg tgctggggct gcagcacaca acagcagcca aggcctgat 720
gtccgccttc tacaccttc gctaccact gagctcagc ccagatgact gcaggggcgt 780
tcaacaccta tatggccagc cctggcccac tgtcacctcc aggaccccag ccctggggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcttttgacg cggctctccac catccagggc gagctctttt tcttcaaagc 960
gggcttttgg tggcgccctc gtgggggcca gctgcagccc ggctacccag cattggcctc 1020
tcgccactgg cagggaactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccagag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccgagg cgtgtagaca gtcccgtgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgtgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc cccgtctcgt 1440
gggtcctgac ttctttggct gtgccgagcc tgccaacact ttcctctgac catggcttgg 1500
atgccctcag ggggtgctgac ccctgccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtgggggtac aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg cagggaggct ttggcatgac tt aagaggaa gggcagtctt 1740
gggaccgct atgcaggctc tggcaaacct ggctgccctg tctcatccct gtccctcagg 1800
gtagcaccat ggcaggactg ggggaactgg agtgccttg ctgtatccct gttgtgaggt 1860
tccttccagg ggctggcact gaagcaaggg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggctgtaggg cagggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggggtattct catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcggggct gtggccagnt tgcctcacgg aggtgcaggt aggtcggggc ctactaggg 240
cancctggagg agcacggact gccctgccgg cag

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac ttgtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```

224/292

```
cctcgcacatc tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagccngg tgaagnacca 330
```

<210> 349
 <211> 1168
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1168)
 <223> hypothetical protein mgc13071 (MGC13071)
 gene.

```
<400> 349
aaatgatgat agtagtacct acagtatagt gctgtagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcatcctct tccggcccat cactagccag cttcctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcctcaagtc actggtggct cgctttgatg ctggagaact aatcaccagc agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacccttggg ctcattctgg 600
acgacgtgtc ttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcggcagat ttgtggtgga aaaggcggcc atcatctctg ctgaggggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggacg gccagagcga 780
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gcccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgtaaca ccacctttcg 960
ccctacccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaa aaaaaaaaaa aaaaaaaa 1168
```

<210> 350
 <211> 315
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(315)
 <223> 5' terminal sequence. interleukin enhancer
 binding factor 2, 45kd (ILF2) gene.

```
<400> 350
ctggtcttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
ccaatcttc gaaaactgga tccagaactc catttgata tcaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctgggtc gaggaatg cttctcagtc cacagttaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240
```

225/292

ccnnggatnc ttgaactact aggnccattat gctgtgatga acaacccac caganagcct 300
ttggcnctaa acgtt 315

<210> 351
<211> 1552
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1552)
<223> interleukin enhancer binding factor 2, 45kd
(ILF2) gene.

<400> 351
cggttggtgc ggcctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
ggtcgtggtg ggcgcttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180
cctgatgaaa ctctcttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
tctgtgaac aggcattctat cctttctctg gtgacaaaaa taaacaatgt gattgataat 300
ctgattgtgg ctccagggac a tttgaagtg caaattgaag aagttcgaca ggtgggatcc 360
tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgt gatactcaag 420
attctgccaa cgttgaagc tgtgtctgcc ctggggaaca aagtcgtgga aagcctaaga 480
gcacaggatc cttctgaagt ttttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600
gatccagaac tccatttgga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
gcccgtggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
aaggacttga ggattcggtt tcttggttt gagccctca c acctggat ccttgacct 780
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttggccct aaacgttgca 840
tacaggcgct gcttgcagat tctggctgca ggactgttcc tgccaggttc agtgggtatc 900
actgacccct gtgagagtgg caactttaga gtacacacag tcatgaccct agaacagcag 960
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020
aagatccttg gccaggaggg tgatgccagc tatcttgctt ctgaaatatt tacctgggat 1080
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
aactcaggag tgacattccc ttactcctt ttctaccga agggaaagac tggagcctaa 1260
gctgcctgct actggcttta catgttgaca gacattccgt ggataggaag atagcaggag 1320
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500
aatgttaagt gtctggaaat ttttttttct aagaaaaact attaaagtac tt 1552

<210> 352
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(396)
<223> 3' terminal sequence. hypothetical protein
flj11307 (FLJ11307) gene.

226/292

<400> 352

```

ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
gggtactggag gtttcagttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcatc 180
aaagcctggtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttggg ttgtcctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcncat tagtggcatt ccataa 396

```

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307) gene.

<400> 353

```

tcgatgaaag atcctccgga cttattggac aggagaaat gcccgaaagc cttggcgtct 60
cttcgacatg ccaaatgggt tcaggcaagg gcaaatggat taaaatcatg tgtaat tgtc 120
ctccgcattc tgcgtgattt gtgcaacaga gtcccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggccttga gacgagtaat ggagtgttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagacca acag atgctc tgagctatat gaccatccag 360
caaaaagaag atattacca cagtgcacag catgcaactc gactatcagc ctttggccag 420
atttacaaag tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagcta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc cccgttcatg cccagctctt cacaatgtct 720
gtagatgttg atggcacaaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780
cacgtagcgg tgaaggattt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgcttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcaggaggc cagggtccaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaagggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcttatgg tttacccaag agaatggttc tgttac ccgt tatgaaattt 1440
ccaacatatt ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagtttaa gtttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgatc acaataaac tgctttgttg taacacag 1858

```

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

agaaccccg ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt 242

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene

homolog (MYB) gene.

<400> 355

ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcgggagggc 60
ggcaccgccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccccg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg ctccccaagt ctggaaaagcg tcacttgggg aaaacaagggt 240
ggaccgcggg agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaagttat tgccaattat ctcccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccttggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacgggtccga aacgttggtc tgttattgcc aagcacttaa 480
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accactggaa ttctacaatg cgtcggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttccagaa gaacagtcac ttgatgggtt 780
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gtaccccggt gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagt 1140
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tggaataatg taagaacctc ttagaatttg cagaacactc ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaat gccttcttta acttccaccc 1380
ccctcatttg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaaccg cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaactg cacttgcagc tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620

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aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt caccgagacc tcgcctgtgc 1800
gagatgcacc gaatatctctt acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
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tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgggtt acaacagttg 2160
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gttaatatct taatgcagat ttttttAAAA a aaacataa aatgatttat ctgggtatttt 2340
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gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
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<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

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gtagttaaat gcagaaagtc ggtttttttc cacccttttc ctctttttac acggcaagta 60
aagctcactg gcctgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgctgca gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaattc tcccacaaga atancccttc 360
tgctcanct 369

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<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1500)
 <223> zinc finger protein 9 (a cellular retroviral
 nucleic acid binding protein) (ZNF9) gene.

<400> 357
 gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggcctgcgtc cgagtctccg 60
 ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
 ttcaagtgtg gacgatctgg ccactgggcc cgggaatgtc ctactggtgg aggccgtggt 180
 cgtggaatga gaagccgtgg cagagggtgt tttacctcgg atagaggttt ccagtttgtt 240
 tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctggtcatct tgccaaggat 300
 tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
 tgcaaggagc ccaagagaga gcgagagcaa tgctgtctaca actgtggcaa accaggccat 420
 ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttgtgg agaattcgga 480
 cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tgggtcatgta 540
 gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcaggggcac 600
 cttgcacggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgccctcct 660
 tttctgatt gatggttgta ttattttctc tgaatcctct tcactggcca aaggttggca 720
 gatagaggca actcccaggc cagtgaagct tacttgccgt gtaaaaggag gaaaggggtg 780
 gaaaaaacc gactttctgc atttaactac aaaaaagtt tatgtttagt ttggtagagg 840
 tgttatgtat aatgctttgt taaagaacct cctttccgtg ccaactggtga atagggattg 900
 atgaatggga agagttgagt cagaccagta agcccgtcct ggggttcctt aacatgttcc 960
 catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
 ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080
 catctgtatc aggccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
 atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200
 tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260
 caaagactaa atctaaaacc cagagtaaac atcaatgctc agagtttagca taatttggag 1320
 ctattcgagg attgcagaga aatgcatttt cacagaaatc aagatgttat ttttgatac 1380
 tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaaag tcaga tggaa 1440
 agagcaactg aagtcctaga aaatagaaat gtaattttta actattccaa taaagctgga 1500

<210> 358
 <211> 425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(425)
 <223> 3' terminal sequence. camp responsive
 element modulator (CREM) gene.

<400> 358
 ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaagt 60
 tcagatattt aaatgagcac caaacactac aaagtgcaac caacatggtt ctattaaaaa 120
 ctcnctttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
 actaatataa aaatctgcaa atgccatata ttcatatcta ggctattctt cncatatagg 240
 catgtcatta gatagacttt ctttctattc ttccngagg natttttttg nggtttacnt 300
 ttattgnact gctggtatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
 gcaaataatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
 gtggc 425

<210> 359

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<211> 232
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(232)
 <223> 5' terminal sequence. camp responsive
 element modulator (CREM) gene.

<400> 359
 ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
 agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
 gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
 tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
 <211> 1431
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1431)
 <223> camp responsive element modulator (CREM)
 gene.

<400> 360
 atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttagacagag 60
 agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
 tgcagtgaagc tgagatcagg caccagaaga ggctccccag ctgtaactct agtgcagtta 180
 ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
 cagtcattcag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
 gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagacctct 360
 tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
 gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
 atatattcaga ctgacacggg gcaatacatt gctatagccc aaggtggaac aatccagatt 540
 tctaaccacg gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600
 gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
 cagttctttg tcccaggcag ccaggttggt gttcaagctg cactggtga catgccaact 720
 taccagatcc gagctcctac tgcgtcttg ccacaggag tgggtgatggc tgcacgccc 780
 ggaagtttgc acagtcccca gcagctggca gaagaagcaa cacgcaaagc agagctgagg 840
 ctaatgaaaa acagagaagc tgcccgggag tgcgcagga agaagaaaga atatgtcaa 900
 tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960
 aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
 ttactctaa tcaaggcagg agatgcagca gtcctactta ttgccatgtg gacttgtggg 1080
 aaggacacgt gtgacctta agaattcagt ttggattagt gtttgaatt gaattgggaa 1140
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 tgtcaatagc atgcaaaaaa tgcctttgtt gccctttgct tctgcttttt ttcagggaag 1260
 ctgcaaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
 cagtgtctga agtccagaac aagaagctta tagaggaact tgaaaccttg aaagacattt 1380
 gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

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<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca ggggaagct 60
gtaatttttc aaaaacagta aaagctggtt tctcctaaac tattttcctt gtgtagtag 120
agatcagtg gtcagaaaca actcctgacc acttggttcc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacaggcttc ccgctgttcc actggctcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggttgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggctccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gagggtactgg gggaactgat ggggaactt tcac cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta ggggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgct g gcncttaagg 240
tgaataaggt ggtggtgact gttctgcaga gagtttctca taagcagggt gagcattggg 300
aaccacaggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttctctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363

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attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatgttta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcggcat cctgacagtg atcctgggag tcttactgct catcggctgt tggatttga 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc                                     370

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<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

```

agcagacaga ggactctcat taaggaaggt gtccctgtgcc ctgaccctac aagatgccaa 60
gagaagatgc tcacttcac tcattgttacc ccaagaagg gacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgtcga 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300
acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt ggtccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcaccttaa gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tcctttggaa tgggttagga aaaatgcaag ccatctctaa taataagtca 540
gtgttaaaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggatttctg 720
gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttcga 780
accttgaccg acatgaactg tacacagaat tgttccagta ctatggagtg ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaagatcc 960
tatagctctt tttttttgag atggagtctc gcttttgttg cccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgcct cccagggtca agcaattctc ctgccttagc 1080
ctcctgagta gctgggatta caggcgtgag ccactatgcc tgactaattt ttagtattta 1140
gtagagacgg ggtttctcca tgttggtcag gctggtctca aactcctgac ctcaggatgat 1200
ctgcccgcct cagcctccca aagtgtctga attacaggcg tgagccacca cgcctggctg 1260
gatcctatat cttaggttaag acatataacg cagtctaatt acatttctact tcaaggctca 1320
atgctatttc aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg                                     1524

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<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggt aggtttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgttagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttcgcagttg aacaatgatc actgatcaca aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac ccccaggggg ctggcctcag atctacctaa 540
ggggnnggat aacccc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60
cgtcagcaca gcatcttttg agatccgaag aagatcgta cagaagagtt tgtgcgcaga 120
gggtacctga tttataaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaaggggt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300
gagggttagg ctatcctcaa ttcagggtgt aggggttatt ccgcccctta agtagatctg 360
gaggcagacc cttggggggt gtaaaagaga gtnacaggta ccccaaagg agtagatg nc 420
aaggggcct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcy gcaagtgtcy gcggcggcty ctgcgcgaag tcagctggcy tgggaactac 120
cctttgtagc tgagaacgcy ttgtttattg ctacaaagac tctattgaca ttggtagctt 180
cagcggcagc agcttct tac ggtataaagc tggtgcttcc tgaaggagct acaagcatcc 240

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcactgcca agcacaaaag ccttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tgggtctgga agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag aggggtacctg 720
atttataaac cgggtgcccc tagcagtcgc gtggagtagt agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actggccttg taattatgac tgggattcgg acgatgatgc agagggttgag 900
gctatcctca attcaggtgc taggggttat tccgccccct aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttataa 1140
ttccgtttgt tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgttca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttccgattgc ttatca 1476

```

<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaaatca caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat caggggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcctt ctctacttgg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttcaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 369
 gggtgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
 ccgctctctc cgctattact atgaaaaggg catcatgcag aaggtggctg gagagcgata 120
 cgtctacaaa tttgtctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
 gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
 gacccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
 ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
 agcagttccc attcagggca aacaagnngc agtggngttt gtt ttgtgtt tttt 414

<210> 370
 <211> 249
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(249)
 <223> 5' terminal sequence. cd69 antigen (p60,
 early t-cell activation antigen) (CD69) gene.

<400> 370
 ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
 tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
 atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
 aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
 cccngacgc 249

<210> 371
 <211> 1702
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1702)
 <223> cd69 antigen (p60, early t-cell activation
 antigen) (CD69) gene.

<400> 371
 agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
 tagggaatct tgagaataaa gatgagctct gaaaattggt tcgtagcaga gaacagct ct 120
 ttgcatccgg agagtggaca agaaaatgat gccaccagtc ccattttctc aacacgtcat 180
 gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtggtctt catcaccatt 240
 ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
 ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggctaccag 360
 aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
 tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
 cgatacgag gtagagagga acactgggtt ggactgaaa aggaacctgg tcacccatgg 540
 aagtgggtcaa atggcaaaga atttaacaac tggttcaacg ttacaggggc tgacaagtgt 600
 gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
 tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
 actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780

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```

ttgtgaaaaa aaatattata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgcatgag ctagaagcat 900
cacagggtga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcattgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta ttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatatat ctttgccttt ataactcttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatagtgt atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa 1702

```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21) gene.

<400> 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatgggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgccnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cgggtaccg gcc ng 585

```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21) gene.

<400> 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

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```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gaggttccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaag acaggtaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcatcagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatc aggaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g 451

```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c tttggtgtc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca ccccaacccc 240
caacctcagt ggaaagcaat gccagggat taggctatgg aagggcaaaa tggaccatt 300
caaatttcct ccaggggacc aggccctatt aaccctggga aatgtcctta gctggtggg 360
gaaaggtttg cgattcagga atacatatgt gtatgttttg ttagaagcca tccatagcac 420
acccg 425

```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```

ggcgttccag ttcccacttg gaggccttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aataggcct ggtccctggg aggaaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctggc attgctttc actgaggttg ggggttgagg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaaagct attta tctgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaattttt aaagttactt ttgtcagagg caccaaaggg 420
tttaaactga ttcataaata aatatcngga cttcctcgat cttccaaaaa aaaaaaaa 478

```

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<210> 376.
 <211> 1794
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1794)
 <223> cd44 antigen (homing function and indian blood group system) (CD44) gene.

<400> 376
 cccgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcag ca gcctgggg 60
 actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
 aggtgtattc cagctggaga aaaatggctg ctacagcatt tctcggacgg aggccgctga 180
 cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
 catcggattt gagacctgca ggtatgggtt c atagaaggg catgtggtga tccccggat 300
 ccacccaac tccatctgtg cagcaaaca cagaggggtg tacatcctca catacaacac 360
 ctcccagtat gacacatatt gcttcaatgc ttcagctcca cctgaagaag attgtacatc 420
 agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480
 tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
 caaccctact gatgatgacg tgagcagcgg ctctccagt gaaaggagca gcacttcagg 600
 aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
 gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
 tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
 aggtggagca aacacaacct ctggctctat aaggacaccc caaattccag aatggctgat 840
 catcttgcca tccctcttgg ccttggcttt gattcttgca gtttgcatg cagtcaacag 900
 tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
 ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcat 1020
 ggtgaacaag gagtcgtcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
 cctgcagaat gtggacatga agattgggtg gtaacaccta caccattatc ttggaaagaa 1140
 acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
 actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
 tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
 cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380
 ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440
 tccccacca gctaaggaca tttcccaggg ttaatatggc ctggtccctg ggaggaaatt 1500
 tgaattgggtc cattttggcc ttccatagcc taatccctgg gcattgcttt ccactgaggt 1560
 tggggtgtac tagttacac a tcttcaacag accccctcta gaaatttttc agatgcttct 1620
 gggagacacc aaagggtgaa gctattttatc tgtagtaaac tatttatctg tgtttttgaa 1680
 atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740
 gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
 <211> 452
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(452)
 <223> 3' terminal sequence. cyclin -dependent kinase inhibitor 3 (cdk2 -associated dual specificity phosphatase) (CDKN3) gene.

<400> 377

```

ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggttt catttcaata caaattatgc tagagaactg acatttcaga catgggcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgcctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaat t aaggcagg t gtaagcnc tccattattt 420
cacagcagct ggccatgtcn ggagtcctcc ca 452

```

<210> 378

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. cyclin-dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378

```

ggcacgagcg gcaactggtc tcgacgtggg gcggccanga ctgaagccca ngtnctcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggt gtaaatttaa agatgttaga agaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt ttctgcacc agaggggaac tgtcaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcaccc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

```

<210> 379

<211> 639

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(639)

<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379

```

atggagccgc ccagttca at acaaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccagg t gtaaat tta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt ttctgcacc 240
agaggggaac tgtcaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcaccc atcatcatcc aatcgcagat ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

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tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tcctactata cctgtctgac 480
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
cagaccatca agcaatacaa ttatcttcat gagtctcgga acaaattagc tgcacatcta 600
tcatcaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
attggatcaa ctatttcttc agatcggtct gattcagagc gagaggagat tgaagtggat 120
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgccca 240
gtgtcaaact ttcattcact tcatagaacc cagcatgaca taacagtgcg gggaaaatat 300
tcaatggggc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
aaaacaaaac aaaacaaaac aaactatctt tgaacaaaag ggtcagagga ctgttttaag 420
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgcctgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60
ttcctttttt tttttttttt ttttaagtaat taagggtagt taaattatth aaagtataca 120
aagtccaaac agccaggggt aagggtctcca agaggccttc ccagggttaag ggagtgcgga 180
gaggcccccg tcgccaccg cggtgcccat ggagcgggtg aagatgatca acgtgcagcg 240
tctgctggag gctgccgagt ttttgagcgc ccgggagcga gagtgtgaac atggctacgc 300
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc caggagggtt 360
gagccgggca cagaaacaca gcagcgggac gagcaacacc a gcactgccca acagatctac 420
acacaatgag ctggaaaaga atcgacgagc tcattctgcgc ctttgttttag aacgcttaaa 480
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
gaatttgtaa cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctctca 660
ggagatggaa cgaatacgaa tggacagcat tggatcaact atttcttcag atcgttctga 720
ttcagagcga gaggagattg aagtggatgt tgaagcaca gatttctccc atggagaagt 780
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 8 40
tgggagtgac gagggttact ccagtgccag tgtcaaaact tcattcactt catagaacct 900

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agcatgacat aacagtgcag ggcaaaatat tcaatggggc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatc agtctcctct ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgacaaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttggtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcacta cattgagtag acacatttaa 1260
ggatgggggt atgaaccctt cctgagcttt atggctcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgatc aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctc gcaaaaggag agactcccat ga agcctttt 1500
gaaaggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaaccct 1560
atcctgcatt gttagcacta ggcaccagc tgccacctct ccatcctgct gcccttaggc 1620
cacatgggag cagtcctatc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
gggggggcaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aaccaaattg acatctttt aaagcttctc cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat tttgatgcag 1920
catttgataa tgataaaaaa cctcacacct cactctttat agtcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccactctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcactgt ctcattttaa tgtaaagatt tgcttcatt ttcctacagg cagtctctct 2160
cttctcaca gtccactgt gcaggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcattgtgt ccttttgtct 2280
ttcaaactcc aagggtcccc tgtggccctc tcccttacc tggaaggcc tcttgagagc 2340
cttaccctg gctgtttgga ctttgtatc ttaaaataat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa 2416

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5)
gene.

<400> 382

tttttttttt ttgttatagt tacttcaagt aacacagctt gttcatata aataagttaa 60
aacatctatt ttttttcaag acaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgcata atggcaataa acaggctcat gattaaaaa tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggatc cgctaaatac tgctcagtag tttaaacgct cagatactca 300
gggacggaag gccctcctt gccgcggnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
 <222> (1)..(439)
 <223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383
 aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
 cgctatccaa atggcccga ctaccagttg cataattatg gagatcatag ttccgtganc 120
 gagcaattca gggactcggc gagcatgcac tccggcagggt acggctacgg ctacaatggc 180
 atggatctca gcgtcggcng ctcngctcc ngcactttgg ctccggagag cgcgcccgca 240
 gctacgtnc agcggcacgc ggcncactcc aagcccagggt acagcnagcc ggccacgtcc 300
 acgcactctn cctcancnec atccgctgcn ctgtcccgnc gtngggccct tcgcccngga 360
 ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgcctcgggc 420
 cgacngccgg aagcaccca 439

<210> 384
 <211> 813
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(813)
 <223> homeo box a5 (HOXA5) gene.

<400> 384
 atgagctctt attttgtaaa ctcatcttgc ggctcgctatc caaatggccc ggactaccag 60
 ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
 cactccggca ggtacggcta cggctacaat ggcattggatc tcagcgtcgg ccgctcgggc 180
 tccggccact ttggctccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcggcg 240
 cccgccgagc ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
 ctgccctgct ccgccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360
 tccctaagca actccagcgg cgctcggcc gacgccggca gc acccatat cagcagcaga 420
 gaggggggtt gcaeggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480
 agtgcgcaga gcgagccgag cccggcgccg cccgcccac cccagatcta cccctggatg 540
 cgcaagctgc acataagtca tgacaacata ggcggcccgg aaggcaaaag ggcccggacg 600
 gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
 accgcagaa ggagattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720
 atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
 atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 3' terminal sequence. x-box binding protein 1 (XBPl) gene.

<400> 385

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```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaataac ccttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttctacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgctc

```

447

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 386

```

aagaacctgt agaagatgac ctcggtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttcccttcc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag

```

462

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

```

ggcgctgggc ggctgcggcg cgcgggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaaccgcgc cgacgggacc cctaaagtcc tgcttctgtc ggggcagccc 120
gcctccgcgc ccggagcccc ggccggccag gccctgccgc tcatggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgagc tggaacagca agtggtagat 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggcctttagt ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctggttgct 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtcc 540
gcagcactca gactacgtgc acctctgcag caggtgcagg ccagttgtc acccctccag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatcctgt 660
tgggcattct ggacaacttg gacccagtca tgttcttcaa atgcccttcc ccagagcctg 720

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ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggagc tcatcagcca agctggaagc cattaatgaa ctaattcggt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaac gaggaagcac ctctcagccc ctgagagaat gatcaccctg 960
aattcattgt ctgagtgaag gaagaacctg tagaagatga cctcggtccg gagctgggtg 1020
tctcaaattc gctttcatcc agccactgcc caaagccatc ttctgccta ctggatgctt 1080
acagtgaact tggatacggg ggttcccttt cccattcag tgacatgtcc tctctgcttg 1140
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tctaaggaa gatccaatac tgttgccctt ttccttgact attacactgc ctggaggata 1260
gcagagaagc ctgtctgtac ttcatcaca aagc caaaat agagagtata cagtcctaga 1320
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gcagccaag gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
acagctttta agattgtact tttatcttaa aagggtggta gttttcccta aaatacttat 1500
tatgtaaggg tcattagaca aatgtcttga agtagacatg gaatttatga atggttcttt 1560
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tgcttctgta agcaacggga acacctgctg agggggctct ttccctcatg tatacttcaa 1680
gtaagataca gaatcttttg tgaaattata gaaatttact atgtaaat gc ttgatggaat 1740
ttttctctgc tagttagct tctgaaagg gctttctcca tttatttaaa actacccatg 1800
caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaatgtt gactcttggtg aaaagttaca tttatttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaatgtgc 120
aaatttcaaa tactttttat aataagtata aataattact tttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttaa gagaattaga tgaaaacact 240
gaagttttat tngtatcct tggaaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggccnt agtacagac cccnnaatg gcagccttta tcnccgggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

```

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatnngnn cctctt                                     206

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<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

```

tgccttgacc aggacttggg actttgcgaa aggatcgcg ggcccggaga ggtgttggag 60
agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat gcgaaagct 120
gtgaagatac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
cattttaaaa ccatgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtag tgaggaaggc gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaataca catatttgc 660
ctttgcaaca tctcagaag gccaatcatt gtcatttcag acaaaatgct aagaagtttg 720
gaatcaggtt ccaatttcgc ccccttgaaa gtgggtggaa tttacttgcc tctccactgg 780
cctgccagg aatgctacag ataccocatt gttctcggt atgacagcca tcattttgta 840
cccttggtga ccctgaagga cagtggcct gaaatccgag ctgttccact t gttacaga 900
gaccggggaa gatttgaaga cttaaaagtt cactttttga cagatcctga aaatgagatg 960
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aacacgagc aggggaggag agaggggcac gccagaatc ccatggaacc ttccgtgcc 1200
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aggagcccc gctgccctt cactgaat gtgcagcaca a cggattttg tgaacgttgc 1560
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gggaagtgcc aagcctgcct ccaggatgt accaggacat ttaatgggat ctgcagtact 1680
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cccaaccaga ggatggggcc tggggccac cggggtgagc ctgccccga agaccccccc 2340
aagcagcgtt gccgggcccc cgctgtgat cattttggca atgccaagtg caacggctac 2400

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tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaacacagg tgggtcacct 2460
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cctttcttga ggaccggca gaaatgcaga accatccatg gactgtgatt ctgaggc tgc 3060
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taaaaaatta gaatttttta ctgggaagac gtgtaactct ttgggttatt actgtcttta 3180
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ttaatgtgaa aaaaagtaat tatttatact tattataaaa agtatttgaa atttgacac 4320
ttaattgtcc ctaatagaaa gccacctatt ctt tgttga tttcttcaag tttttctaaa 4380
taaagtgaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

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<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

```

tttttttgtg cacaaaaatg atacatttat tgaaagagta tttttttttt aatacaaaaag 60
aaagctctgt acataggact gtgacctgt ccaactattcc tgggtcagca tcccagggga 120
agtagaaaacc actgacatac aactcacat tcaagcacac aactcactc aggcgcacac 180
accacacacac acatacccca gagccaccga ggaagggaac caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgcatgtcc tcccaaggcc acgtcacac 300
aacacacatt ataagcactt tgcttgattc actcactnng gtctgtcttt tgtgggaagg 360
agaggaagaa ttcacaaag gtctcctccc catgggtngg gggagtgggg agtgagtga 420
tgatggtgga gtgaaacaag

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<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60
tgcagcaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaatt aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taattttgtac aggggccatg ccacncccc tctctcccct ttngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatttt 360
cttaaccctt aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
ggtcggggga tccctccgcc gccagcgcgt ggtcccggcc cctccaccc gccgtctcgg 60
ccgcggccag cagcccctgc cccccgggg acgctgacgg ccgcccggcg cgccgcccta 120
gcagacggac agggggcgct gcgcgcggcc tggggcaacc cgggccac ag gggcaggaaa 180
gtgagggccc aggtcggccc gggcgtgcag gggccccggg ttgcagcgg cgcccgggc 240
agcgatagcg gactagcag cagcgggagt gccgggtga gccgggaagc cgatggcggc 300
ggctgcggcg gctccgattc ctcgtgact gccgtccgc cctcctgcat cgagcgccat 360
gttaccgacc caagctgggg ccgcgg cggc tctgggccgg ggctcggccc tggggggcag 420
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gggcccggtc cccgggaatg gcgcggggct cgggcccggc cgcctggagc gggaggctgc 540
ggcagcggcg gcaaccaccc cggcgccac cgcgggggcc ctctacagcg gcagcgagg 600
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cgggggctac gggcgggtga ggcggcggt gagcggggc aagccgggta agaagaccg 780
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acagggtgct ttgctggtgg ccagtgcagc aggccatgtg tatacctttg ccaccgaaa 960
actgcagccc atgatcacca gtgagaccgg caaggcactg attcagacct gcctcaactc 1020
gccagactct ccaccccggt cag accccac aacagaccag agaatgagtg ccaactggctt 1080
tgaagagaca gatctcacct accaggtgtc ggagtcgtgac agcagtgagg agaccaagga 1140

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cacactgaag ccggcggttca cagtcaccaa cctgccgggt acaacctcca ccatccaaac 1200
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 ctacctggca ccagtgtctg ctagtgtcag cccagtgct gtcagcagtg ccaatgggac 1320
 tgtgtgaag agtacaggca gcggccctgt ctctctggg ggcttatgc agctgcctac 1380
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 gcaggtgtca cacagccagg tccaggagcc aggtggcgct cccaggtgt tccctgacagc 1740
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 g 4201

<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(563)
<223> 3' terminal sequence. sry (sex determining
region y)-box 9 (campomelic dysplasia, autosomal
sex-reversal) (SOX9) gene.

<400> 394
tttttaatgc aatgtatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaaa ggtaagtttc acggagagaa caaaagggtt ggggctggga gggaaacaag 120
tgaacacaaac aaaacacgaa cacaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgtttta agattttatt ctactgactt ctaaaactgt 300
taatatactt ttttttaaata aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atcccccca 420
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttgtg nccaaacaca cacanacca nacacacna caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa 563

<210> 395
<211> 3936
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3936)
<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395
ggagagccga aagcggagct cgaaactgac tggaaacttc agtggcgcg agactcgcca 60
gtttcaaccc cggaaacttt tctttgcagg aggagaagag aagggtgca agcgcccca 120
cttttgcctc ttttctctcc ctctctctcc tctccaatto gcctccccc acttgagcg 180
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggt gccggc cgac 240
gcgccagctt ccccgggagc cgcttgcctc gcatccgggc agccgagggg agaggagccc 300
gcgcctcag tccccgagcc gcgcgcgtt ctgccttcc ccggccacca gccccctgcc 360
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ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgcccg 480
tcgggctccg gctcggacac cgagaacacg cggccccagg agaacacgtt cccaagggc 540
gagcccgatc tgaagaagg gacgaggag gacaagtcc ccgtgtgcat ccgcgagggc 600
gtcagccagg tgctcaaagg ctacgactgg acgtgtgtgc ccatgccggt gcgcgtcaac 660
ggctccagca agaaacagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggcg 720
caggcggcgc gcaggaagct cgcggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc cttcgtggag 840
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cggcggagga agtcggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaacgccc cttcaaggcg ctgcaggccg actcgccaca ctctctctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080
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ggcagctacg gcacagcag caccgcggcc acccggcgga gcgcgggcca cgtgtggatg 1380
tccaagcagc aggcgcggcc gccaccccc cagcagcccc cacaggcccc gccggccccg 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcgggcacc cccgcagcag 1500
ccacaggcgc acacgctgac cagcgtgagc agcagagccg gccg gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgcgcccaa 1620
cagatcgccct acagcccctt caacctccca cactacagcc cctcctaccc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcggca 1740
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cctttggaca tttgtgtttt tttgtttttt tttttgttt tgttttttct tcttcttctt 2040
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atggagcagc gaaatcaacg agaactgga ct ttttaaac cctcttcaga gcaagcgtgg 2220
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gtaagcttta tgatatatat attttttaaa gaagagaaaa acaccttgag ccttaaaacg 2760
gtgctgctgg gaaacatttg cactctttta gtgcatttcc tctgccttt gcttggtcac 2820
tgcagcttta agaaagaggt aaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
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ttgttctctc cgtgaaactt accttccct ttttcttct cttttttttt ttgtatatta 3900
ttgtttacaa taaatatata tt gcattaaa aagaaa 3936

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<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

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tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tggaggagg caaaggtggg actaggagg 120

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251/292

tgaccgcgat gggccagatn ggagagaaac ttttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgccgccac ttgcagaga tgccccgcag ncagcctgca cccccagcca ccccgagtgc 120
tgcccaccag ccccttgac atcgccgact tcatcaatga tggcttgga g gctgcagata 180
gtgaccccag tgtgccgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cgggtggcggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggtct ttctcctggg 420
gcactgctac ccagacacag aggcgggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgcgctg tcaactcagcc tggacgcgct tcttcgggtc gcgggtgcac tccggcccgg 60
ctcccgcctc ggccccgatg gacgccgcgt tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccaccctg taccctggc 180
gccggggcgc tgccctgagc cgcgtgcgga gggcctgggt catcccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtcggac aagcagcagc 300
tgggcagcgt catctacagc atccaggac ccggcgtgga tgaggagccc cggggcgtct 360
tctctatcga caagttcaca gggaaggctc tctcaatgc catgctggac cgcgagaaga 420
ctgatcgctt caggctaaga gcgtttgcc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttctgcagg 540
aggcggtcac tggccgcgct ctggagggtg cagtcccagg cac ctatgtg accagggcag 600
aggccacaga tggcagacac cccgagacg acaacgcagc gctgcggtc tccatcctgc 660
agcagggcag ccccgagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780
tgtctggaga cggcctcaca gccactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtgatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

252/292

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ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag cccccgtgt 1200
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ccttcctgcc ggggtgggaa gagtttctct ccacggccc catgcgggtc acc tccctag 2760
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<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 399

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tatctcacac tgtactttat ttttcttcac aatattaact agacagacaa ggaaagttaa 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taacctatga aagtatcctt accgtatttt ttatgtgtac 180
agtgttgcag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttcaatata aaaacactta ttgtacactt 300
atttttattht aaacaaaaaa taac cccagt aactcaaaac aaaagcaaac cttggttgaa 360
tacttaagaa ggtataataa aaaaaccac caaagaaaag cttccccaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaataa cttaatgaaa tgagctatct 480
ggaggggccca cggagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctacagantc ctgattgagc gagcctttcc atctccacca 600
gtgtccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

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<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 400
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ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataatata agtccttttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataaact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
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tgacacagct cctgggcacg cctgctgcgn gtncgcttcc catga ccccc agggccctct 120
atgcctcccc cccagggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggtc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

254/292

1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402

```

tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgagggtct ccgcatttat tttcaaggcc aaaggaagtg 180
accctcggga aaacaccctc gcacaacaaa gggcttcag aatctccatt gcacgagtct 240
cttccacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcaactca 360
gagtatcggg acccaagatg cactattggt gactcctgcc ccaccctggc aacttggcac 420
atggttcctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggtnatttt ggctttttcc ggtcagctgt aaagtittaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggnagggga aanccttt 568

```

<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3), (GZMA)
gene.

<400> 403

```

cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaatt tcctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcaactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaacctgt 480
gccaaagtgc aggttggggg aggactcaca atagtgcac ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaatgaat atggtttgtg ctggaagcct ccgagggtgga agagactcgt 660
gcaatggaga ttctggaagc ctttgttgt gcgagggtgt tttccgaggg gtcacttcct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 840
ttcatttact gtggttctt aatcttttca caaataaa 878

```

<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

255/292

osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404

gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgccccctcg 60
ccccctgccc ggcttttgcta accgccacga t gatgttctc gggttcaac gcagactacg 120
aggcgtcacc ctcccgtgc agcagcgct ccccgcccg gataaactct ctttattaca 180
attaatcanc g 191

<210> 405

<211> 245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405

ttttcaactt aaatgctttt attgacaatg tcttggaaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
ttcatggaaa actgttaatg tcngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245

<210> 406

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(489)

<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406

gcgncgcgct caccgaaggg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaatg tttgccaggg acaaagtcaa 240
cacaagagaaa caaacaacaa aaaatagcca gaaagagAAC agttaagtgc agctcgggtga 300
gtcccggcag ttccttcccgc gactgggtc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgtccg tccacctgtc cagcgagcc acatgtgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgccA gagtagcttc gtctgaactt 480
gaacaagac 489

<210> 407

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

tgttttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcgt ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccagga cgagccagt cgggaagga actgccggga ctcaccganc tgcncttaac 240
tgttctc 247

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

gcccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60
gtctgctcgc tcgccggcgc gcctcgcctc ggccccctcc ctacgctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gcctcggcgc gccaccggcg cccgcgcgga gcggcccggg 180
ggccctcacg caggcccatg gcggcgcgcg ggcgcgctct cgggcccggc accacgcggg 240
cgcgggggcg ggggcgcgg ggcggggggc ggtcccgccg ggcgctgggc cgtgggcgcg 300
ctggagggcc gcgagttcga gtatctgatg aagaagcgt cggtgaccat cggccgcaac 360
tcgtcgcagg gctcgggtgga cgtgagcatg ggcactcga gcttcatttc cggcgccac 420
ctcagatct tcacgcccc gggcgcgcg gccatggcgg ggcgctccg gagctgccgc 480
ccgcgcagcc caggcccgcg gccggcgcg acttctacct gcgctgcttg ggcaagaacg 540
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tgtgcacatt caggttccc agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccccgtac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
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cctcgacctc ccagccacce gtcgtgcaga cggttcacgt cgtccaccag atcccagcgg 1620
tgtcggctac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680

257/292

```

ctgtgggtcac cccggcagcc gtgctggccc ctctaaggc agaggcccag gagaatggag 1740
accacagggga agtcaaagtg aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgccag ccggatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacaggc acctctaggt caacaccagc taccaataaa aactgtaaca caaaacggca 1920
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```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDI) gene.

<400> 409

```

tttttttttt tccttcaggg gcatttatct cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcaactggg cccttggttg ttccctggctg ggtcagggaa 180
ggcctgccgn ggtggtgggc a

```

201

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDI) gene.

<400> 410

258/292

```

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggccctg gttgcccctg gacgtgtgcg 120
tctgctgctc cggggtggan ctggggtgtg ggatgcacgg cctcgtgggg gccgggcccgt 180
cctccagccc cgctgctccc tggccagccc cc ttgtcgt gtcgggtccc tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctactaa gcctctaant cactgtg 297

```

<210> 411
 <211> 1819
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1819)
 <223> rho gdp dissociation inhibitor (gdi) alpha
 (ARHGDI A) gene.

```

<400> 411
cctgaaccgc gcggccgaac cctccggtgt cccgaccag gctaagcttg agcatggctg 60
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actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
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cagaccccga cgtcccacac gtctgtgtga ctggcctgac cctggtgtgc agctcggccc 300
cgggccccct ggagctggac ctgacgggag acctggagag cttcaagaag cagtcgtttg 36 0
tgttgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatatct acaggaaaag cgtcaagatt gacaagactg 480
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aggactgagc ccagccagag gcgggcaggg cagagtgtat gacggaagac ggacaggcgg 720
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ccctcgatgg acaggcctga cccaccccac ctggggccag ccaggagccc cgcctggggc 1560
atcagtattt attgcctccg tccgtgccgt ccctgggcca ctggctggcg cctcttcccc 1620
cagcctctca gtgccaccac ccccggcagc cttccctgac ccagccagg a caaacaaggg 1680
accaagtgca cacattgctg agagccgtct cctataggtc ccccgcccca tcccgggtgt 1740
tggtgttgtg tctgccaggc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

```

<210> 412
 <211> 306
 <212> DNA
 <213> Artificial Sequence

<220>

259/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcataaaag cggacacagc 60
agtgttcca gttcatggt tcccagggtc aggttcctcc cagcggagggt gggagggcag 120
ccctcacacc tggcaccctc gagtgcatac tcctggagga agtcgttgag ctgggcacag 180
gctgcccgct ggcgggtgcn tccggcacag gcgttcagag ggcattcctc cgatccagct 240
attcgagtcc agcaagta ct ngggggggnc cctcccaggg gcataantng gncctccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
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ctctgtttct ctcttctgt ggttcattcg ggg gtcccc tatcgggtgg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg tcttgagaaa cccatctcgt 240
aataatgtcc cctgtctccc aaagggtggac ttcacctta gctcagaaa agacttcgca 300
ctcctcagtc tccagggtgcc cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
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gatcagaaga tgcgcccgag cactgacacc atcacagtca tgggtggagaa ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg cctcgtcca tcttcagga tgactttgtg 660
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<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
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aaccttgagt ctagatttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180
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ggggctggta gagctgggtca ttgggcaac a gagtctgctt gtctgnaagc tctcgactgg 360
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<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
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aaaggatcac agaacaagtc aaaaccactc caagtgtatt acagaatgtg tcaganctgc 240
attgaactaa atgcagccac catatctggc ttctctttg ctgaaatcgt cagcattttc 300
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tcagacaagc agactctgtt gcccaatgac cagctctacc agccctcaa ggatccgagg 420
aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

```
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taaaaaaaaa tggaatctgg gaagtaatgc caaggaccct cgagggatgt atcagtgtaa 300
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```

<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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aggggatggg ggtgctagac atcctgggtt gggattgcac ggctcctcca cctccctccc 360
caccagtgcc ccctcctctg gcacgcgggg gctacgtggc ttcaggcccc gggataggag 420
gccgccccca aaggccgct 43 9
```

<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418

```
acgggggatg cccaacgtcc ttggggagct gaacagtctg gacccccatg gcatcgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccacc accgctcagg 120
cccgcttctc ccgcgcgtcag cctgtctgcc agaccctgac ttcttctctg ggcaccgtgt 180
tccctgcccc gcngggaggc cctggggggc ctgnacctcc tgggacgatg gggt 234
```

<210> 419

<211> 2314

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419

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cccgcccgcc cgggccccgc gtgcatgctt cggctctggc cagcctctgg gccgtccgtc 180
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```

264/292

```

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gttttttgag ctcaaaaaaa aaaaaaggaa ttcc 2314

```

<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 420

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acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcacg ggcaaaaggg 180
catattaatc catcaaacac aatttgcat ttga 214

```

<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 421

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<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6450)

<223> estrogen receptor 1 (ESR1) gene.

<400> 422

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266/292

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gatgtgactc ggttttgcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgactttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

<400> 423

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ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatataccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcaggggaag atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg ttgac tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tctgcccct gccccaactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggagggtat cagagtgaac 420
actgccaggg ccttctgtag gggagggtcac tgatgaaggg gtagtagcat cctgccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

<400> 424

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gccaaagagg agttagccaa gaagtgtggc accacagctct cccaggtatc acaactgggt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa ttcaagagg aagccaatat 120
ttatgctgcc aaaacagctg tcaactgtac caatgtgtca gcccatggaa gccaaagctaa 180
ctcgccttca actcccaact cggtgtgttg atacccttcg ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgctaa 300
tggagggttg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgac tcccagcaat cgcacccgg ctgaccctgt 420
gcccagttg ggcaggggca ggaggaggg tttctctccc aacgctgaag cggtcagact 480
ggaggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1 (PBX1) gene.

<400> 425

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cttccctgtt tctcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccagaccga ggagcagaag aggaagagcc gggggctgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt ccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat ttacagcaa attatgacca tcacagacca gatttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttggtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc ccagctgat gcggctggac aacatgctgt tagcggagg cg tggcgggg 480
cctgagaagg gcggagggtc ggcggcagcg gcggcagcgg cggcggttc tggaggggca 540
ggttcagaca actcagtga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacag caggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagagca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttccga tttctggatg cgcggcgga gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagt aggaagccaa agaggagtta gccagaagt gtggcatcac agtctcccag 960
gtatcaact ggtttgaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
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ggaagccaa ctaactcgcc ctcaactccc aactcggctg gttcttcca g tttctttaac 1140
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agtgtaatg gaggttgga gga tgctact accccttcat cagtgcctc ccctacagaa 1380
ggccctggca gtgttactc tgatactcc aactgatctc ccagcaatcg catcccggt 1440
gacctctgc ccagtttgg gcaggggcag gaggagggt ttctctcca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct tttttttctg 1620
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cctgtgctc tgctctagac ttcccgggt ccccgccctc totcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli -kruppel family
 member gli3 (greig cephalopolysyndactyly syndrome)
 (GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tacttttagg tttttcagag tccttttcca taaa agaat ataattgaaa 120
cacatctcag ttagggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaactc cttcaactcc taatgatttc cgttggttgc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgtg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aacctatgga aaaggtctca atgatacttg 420
ggctcagggc ccgcacatca ggctcgagt gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggtcg 506

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<210> 427
 <211> 239
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(239)
 <223> 5' terminal sequence. gli-kruppel family
 member gli3 (greig cephalopolysyndactyly syndr ome)
 (GLI3) gene.

<400> 427
 ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
 tgtctctatt taataaacaa aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120
 ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
 agagacaggg ttccaccacg ttgccaggg cagtcttgaa ctctgaccc caagtgatc 239

<210> 428
 <211> 5054
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5054)
 <223> gli-kruppel family member gli3 (greig
 cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
 cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60
 gccagatccc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
 tgctccactc gaacagatgt gagegagaaa gccgttgccct ccagcaccac ttctaagtag 180
 gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
 cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
 gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
 ccgtaccgcg ggacgggtt ttgcatggac cccaggaatg gttacatgga gcccactac 420
 caccctctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
 gagggcgtt accattacga tccatctccg attcctc

cat tgcatatgac ttccgcctta 540
 tctagtagcc ctacgtatcc ggacctgccc ttcattagga tctccccaca ccggaacc cc 600
 gctgctgctt ccgagtctcc ctccagccct ccacatccct acattaatcc ctacatggac 660
 tatatccgct ccttgacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
 agccctacag atgcgcccga tgcaggagtc agcccagcag aatactatca tcagatggcc 780
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 acgggggcca tccacatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900
 aggtgtctag ccaggccgag ccgaaaacgt acactgtcca tatcaccact ctccgatcat 960
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 aattcccgtg gca gctcttc agcaagtggc tccatggtc acttatctgc aagtgcate 1080
 agccctgcct tgagcttcac ctactcttcc gcgcccgtct ctctccacat gcacagcag 1140
 atcctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200
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gtccagggtca gctccggcccc ttctgagtc tccacagaaca agcccacgag tgagtctgca 1320
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 ctccccagcc caggggctcg ggggcagcag gaacagcccc aaggaacaac ccttgtcaag 1440
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 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560
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 cgaggggaca tccatcctcg gccgccacc ccgagagatt ccggcagcca ttcacagtcc 2040
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 aacgaagtca gctccggaag cgcgcacctg tcttctcca agtcaagtg tggcccgcg 3600
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 gcgtccctcc cattccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc acctaactga 4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
agggagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaat tttgccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga gtcccggcag 120
ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgtc cagcgagcc acatgtgaa atggaggtgg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTRACTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNGAT GGCNGTGAAT NACTGCAAA 180
NAGCATTGTC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar to NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432
ATTCGGCAGC ATGACTGGCC AGGGTATAAA AAGGGCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTTCCTG TATCCAGGGT TTTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACAGAC GCCTGCCAGG GNATTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTTACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG 247

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT 63

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCCTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG 190

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176).

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTCGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATATA TGCACTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCCACG GNGACATGTG GCCTTCTAGC TTATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTCA AGTAACAGGT GAGNNAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTCTTGA GCTGCAGCTG GCGGTTAGGG CCGGGGCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGNGT 337

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCTCCTG GCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTTCGTCT G GG 223

<210> 443

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<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180
cttcccagan aacctaccag ggcagctacg gtttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggta cagtgaggac 60
cccacagtac ccctgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgaact gctgggtgcc ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aaccccgagt 300
attgacaccc caggggaggg agcttgccct tcagcccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

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<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagagggtg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tocctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcatct tgcgccccct gctggtnгаа 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240
ntcgaagggg ganttgggna ngtagggtnг gtnгcttgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tggtcacaac tataaattta 60
aaccttttgc actaaaaaaa caaaaaacaа caaacacaan accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattotta gcngtcattc agtattttcc 180
tccttgгcaa ctgtaatgtt ttngcaccgg ntgatctccc gcngggggta ctagtaatga 240
ctgгctgccc gtgtagggag atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgnccct gccctactt 169

<210> 448

<211> 393

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 3' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(393)

<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448

aagtaattaa gggtagttaa attatttaaa gtatacaaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggtaaggga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa tttcacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgagggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449

<211> 217

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(217)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(217)

<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449

ttacctgggt atctectact gtagtatgag gaagaatggc tgttaatgta ttttttgaat 60
tctggnctca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120
tgtgccgaga attcctacaa cgagc actgg aactacctga ccatctgccca nctgtgccgc 180
ccctgtgacc cagtgatggg cctcgntga gantgcc 217

<210> 450

<211> 157

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

```
nattcgga cngggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca                               157
```

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis-related cysteine protease
(CASP4) (ex CASP1)

<400> 451

```
gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtctc ctgacagcac attcttggtg ctcatgtctc atggcatcct ggagggaatc 120
tgcggaactg tgcgatgatg gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgect 120
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctogaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggtccttc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttctgt gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaaggtgg gatggggccc agcnacagct ttgnaccc ga gggctnnttg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgecc cggctgcccc tcaccct gtg gcaagtacat ctctgagcc gagtgccctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgggc tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagagggac tcagagggct gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctctg ctggatcatc gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtcc cagtnngaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

281/292

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gttttacgn atgnagtgn aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgnctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggtggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttgacat catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagcaggaac 60
cggcggcggc gngtgcgngt agggccgtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcgggnggca ncanggacga gaaggngnnc accaaggagc tggaccagng 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagnc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccaggnac 30 0
ngnccgngga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456
cagcctcccg cgcctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtcacctg attgctgtct tccagaagta tgctggaa ag gatggttata 120
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggacctt ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatgggtca gctagatttc tcagaatttc ttaatctgat tgggtggccta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360
gggacctggg cctttcaaac ccacccctn ttcctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggacctcgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatggggccc tacagtccct gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tnctaag aacctnaat 359

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

<220>

<221> misc_feature
<222> (1)..(1251)
<223> endothelin 1 (EDN1)

<400> 458
ggagctgttt accccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgctcttgc tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcgcg tgcgcctgca gacgtccgc tcgtgcctt ctctcctggc 180
aggcgtgccc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaacccgc agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgtgtg ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggtgg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cgggtccaagc gctgctcctg ctctgccttg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggaaagcct 600
aggtccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggtcg aagacattat ggagaaagac tggataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaag acaaacagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcag atcccaagct gaaaggcaag ccctccagag agcgttatgt gaccacaaac 960
cgagcacatt ggtgacagac ttccgggcct gtctgaagcc atagcctcca cggagagccc 1020
tgtggccgac tctgactct ccaccctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttactg gcttccatca gtggttaactg ctttggctc ttctttcatc 1200
tgggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251

<210> 459
<211> 2145
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2145)
<223> 3' terminal séquence

<220>
<221> misc_feature
<222> (1)..(2145)
<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459
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ccttcctctc cggaagcccc caggatggtg aggtgggttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggtg gcttctctggc tcggcccagt 240
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tttcttgtgc gtgaga gcct cagccagcct ggagacttctg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc aggggtcacc acatcaagggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgag accttcgaca gcctcacgga cctgggtggag 720

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catttcaaga agacgggggat tgaggaggcc tcaggcgcct ttgtctacct gcggcagccg 780
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catttcgcga tggacagact cacaacctga acctaggagt gcccattct tt tgtaattt 2040
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<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

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caccagggca gccgagagac ctccctcccg cccctcccat gccgcctcc ctccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cggcgtgcc 180
ctttgattcg gatttccatc ttgcattctc cggctgatcg cgggacctgg ct cgtgcaga 240
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agcaacgagc ggagacgcgt gcagagcatc aacgcgggat tccagtccct caagaccctc 480
atccccaca cagacggaga gaagctcagc aaggcagcca ttctccagca gacagccgag 540
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gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcggcagca gctggacaag gagcgtcgg tgcgcatgat gctggaggag 780
caggtgcgt cgctggaggc ccacatgtac ccggaaaagc tcaagtgat tgcgcagcag 840

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gtgatcgtgc cagcaccgac tcctcctccc tcccaccaca tcaatgtcgt caccatgggc 1020
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gcaatccagc acatcgaggg caccagga aagcaggagc tggaggagga gcagcggcga 1140
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ggagaagcta ttatatttt ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
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<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

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gctctccct ccccttccaa aaaacaaaa cagaaaaacc cttttccagg ccggggaaag 240
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<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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tgagggtgat gaacctgatg gagcagccta tcaagggtgac tgagtggcag cagacataca 180
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aggctgcca gagcatgatt cccatcaatg agccctatgg agatgacatg gatgccacct 2220
accgccccat gtactccagc gatgtgcccc ttgaccgct ggagatgac atggacatgg 2280
atggagacta ccccatcgac acctacagcg acggcctcag gccccgtac cccactgcag 2340
accacatgct ggcctaggcg gcctggcccc agtgacggcc ccctctttgc aggcctttcc 2400
tcctctctag aacctccttc tgttggaggc cctcccatct ccccgctgaa acctgcgtc 2460
cttttttggg gggatccttt gctgctgagc ttcccaagc acggtgt gcc ctggcctgcc 2520
ttcttcttgt gtctttggtg gggatgggga ggcctattcc tgctggcccc ttctgggggt 2580
ggtgggcagg tgacacggag tggttgagc ttctggggat gcaggtccac cgagccctg 2640
acctctgtct gtccccgtc ccctaacagg tgcggttct catctgagag gctctccgtg 2700
caggcgatgg ggcaagacag aaaagtgcct gagctgggga agccggggtg taacttcctg 2760
ctgcaccctg cgcctccaga ggtcctccgt agggctcttc ttgggatagt gttctgctcc 2820
tgcttttctg tcctgggcat gggtcaggcg cctgacaccc cctccccgcc cctgtggccc 2880
tggccactaa agcttcagac tcaagtaccc attctgttt cccccagc aa cgccctcca 2940
aacctccagc ctccctgtct ccagctgcct gggcccgaa gggctttggt tccttctctg 3000
ggtctgattt tctcactgaa ctccaccgac caactgccct aagccccag ggcctccagg 3060
gccagggttc gagacccaaa cccccaaaat ccaaaacttc tcttgaaaag ttcaggggacc 3120
gtccagggga gatgg ggagg agatatggag tgagtcacct gctccagaag atgccagctt 3180
ctctctccag ggtgcttagt tggctttgcc caccctcac tcccaggga gctccgggga 3240
cagcttcctc acaccctgt cccaccaca cagctgcct agctgacccc gagaagtgt 3300
cttggctgac ccctctggtg tgtggtgagg ggctttctct tcccttcc t gtttcagacc 3360
ccccatttc ccgcacatgg tgtggggggc tgggggaggt ccaagcagag tgttttatta 3420
ttatcgcttt atgtttttg ttattggttt tttgtatag accaaagcaa agaaaataaa 3480
aataacacag 3490

```

<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
cagtggctgg taggcagtgg ctgggaggca gcggcccaat tagtgtcgtg cggcccgtgg 60
cgaggcgagg tccgggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120
cggctggcac aggaggagga gcccgggcgg gcgaggggag gccggagagc gccagggcct 180
gagctgccgg agcggcgccct gtgagtgagt gcagaaagca ggcgcccgcg cgctagccgt 240
ggcaggagca gcccgcacgc cgcgctctct ccctgggcga cctgcagttt gcaatatgac 300
tttgaggagaa ttctcgctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360
cctggaggaa gtgctcagca aagccctgag tc agcgcacg atcactgtcg ggggtgtacga 420
agcggccaaag ctgctcaacg tgcaccccg taacgtggtg ttgtgcctgc tggcggcgga 480
cgaggacgac gacagagatg tggctctgca gatccacttc accctgatcc aggcgttttg 540
ctgcgagaac gacatcaaca tcctgcgcgt cagcaaccgc ggccggctgg cggagctcct 600
gctcttgagg accgacgtg gcccgcgggc gagcgagggc gccgagcagc ccccgacact 660
gcactgcgtg ctggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720
acttatttgt ttttgccggg aaagtcgcta catggatcaa tgggttcag tgattaatct 780
ccctgaacgg tgatggcatc tgaatgaaaa taa ctgaacc aaattgcaact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900
tgatgccaaag gggctgagtg agttcaacta catgttctgg gggcccgag atagatgact 960
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc ccggggcgcgt ttcgggtgct ggccggctgca gccggagtgc 60
aaacctaaag agctggaagg aacctatggc aactgtgagc gtacctcat tgcgatcaaa 120
ccagatgggg tccagcgggg tcttggtgga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggccgtgtga aatacatgca ctcagggccg 300

290/292

gtagttgcca tggctctgga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360
gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
ggcaggaaca ttatacatgg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
tgacaggagg gcagaccaca ttgcttttca catccatttc ccctccttcc catgggcaga 600
ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gagggaagc 660
tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
cttcctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
agccggaatg gcatggctct gaagcccccac ttccacaagg actggcagcg gcgcgtggcc 120
acgtgggttca accagccggc ccgtaagatc cgcagacgta aggcccgcca agccaaggcg 180
cgccgcatcg ccccgcgccc cgcgctcgggt cccatccggc ccatcgtgcg ctgccccacg 240
gttcgggtacc acacgaaggt gcgcgcgggc cgcggtttca gcctggagga gctcagggtg 300
gccggcattc acaagaaggt ggcccggacc atcggcattt ctgtggatcc gaggaggcgg 360
aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
ctcatcctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480
ctgaaactgg ccaccagct gaccggaccg gtcatgcccg tccggaacgt ctataagaag 540
gagaaagctc gagtcatac tgaggaagag aagaatttca aagccttcgc tagtctccgt 600
atggcccgtg ccaacgccc gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660
gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttggaatc agtcgggcag 720
tcatgctggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780
actgctgtga ctctctcctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
tgataaatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
aaaacggttt tcttgtgggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctctgcagc tggcccccgc 60
ccaggccct gtctccagc ctgatgccc tggccaccag aggaaagtgg tgtcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gtcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggctgctgc cctgacgatg gcctggagtg tgtgccact gggcagcacc aagtccgat 300
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaa ggacagtgt gtgaagccag acagggctgc 420
cactccccac caccgtcccc agccccgttc tgttcggggc tgggactctg cccccggagc 480
accctcccca gctgacatca cccatccac tccagcccca ggccccctctg cccacgtgc 540
accagcacc accagcggc tgacccccgg acctgccgc gccgtgccc acgccgcagc 600
ttcctccgtt gccaaaggcg gggcttagag ctcaaccag acacctgcag gtgccggaag 660
ctgcgaaggt gacacatggc ttttcagact cagcagggtg acttgccctc gaggctatat 720
cccagtgggg gaacaaagag gagcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccgt 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggtgtc cttaagttcc ttgcagcagg aaccactta ggtggacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgtatggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300
tgatgtcagt gttatattct ccaggaatac tggccagagg gctgtgctg a agtttgcctg 360
tgccactgga gccactcaa ttgctggccg cttaactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc caggcttct tggtgttact gacccaggg ctgaccacca 480
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgtgta acacagattc 540
tcctctgcgc tatgtgaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaattgtg tggatgtggt ctgggaagt tctgcgatg cgtggacca tttcccgtga 660
acaccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaaa 720
agaagagcag gctgtgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgt cctgagttca ctgctactca gcctgaggt gcagactggt ctgaaggtgt 840
acaggtgccc tctgtgccta ttcagcaatt ccctactgaa gactggagcg ctcagcctgc 900
cacggaagac tggctgtcag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960
tgactggtct taagctg ttc ttgcataggg tcttaagcag catggaaaaa tggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcacg atgactggcc aggtataaa aagggccac aagagac cgg ctctaggatc 60
ccaaggcca actccccgaa ccactcaggg tcctgtggca gtcacctag tggcaatggc 120
tccaggctcc cggaacgtcc ctgacctgg ntttgnct nctctnactg cctggnttn 180
aanaagctng tgcntccaa ancgtccgt tatccagggt tttgaccac gctatgctnc 240